

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

Amendments to the Specification:

At page 13, lines 16-30, please replace paragraph with the following:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, e.g., <http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/>. Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNN") or the letter "X" in protein sequences (e.g., "XXXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. (Wootton and Federhen, Methods Enzymol 266:554-571, 1996) (~~Wootton and Federhen, Methods Enzymol 266:554-571, 1996~~).

At page 23, please replace Table 1J with the following:

Table 1J. BLAST results for NOV1a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13569928 ref NP_112217.1 NP 112217	a disintegrin-like and metalloprotease with thrombospondin type 1 motif, 12 [Homo sapiens]	1593	269/616 (43%)	371/616 (59%)	e-135
gi 11493589 gb AAG35563.1 AF163762.1 (AF163762) AAG35563	zinc metalloendopeptidase [Homo sapiens]	1077	253/624 (40%)	359/624 (56%)	e-128

Applicants: Guo
U.S.S.N.: 09/981,151

gi 10645199 ref NP-055087.1 NP 055087	a disintegrin and metalloprotease with thrombospondin motifs-7 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 [Homo sapiens]	997	247/571 (43%)	344/571 (59%)	e-127
gi 15309931 ref XP-054419.1 XP 054419	a disintegrin-like and metalloprotease domain with thrombospondin type I repeats 10 [Homo sapiens]	854	245/604 (40%)	348/604 (57%)	e-124
gi 7656869 ref NP-055088.1 NP 055088	a disintegrin and metalloprotease with thrombospondin motifs-6 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 6 [Homo sapiens]	860	244/630 (38%)	345/630 (54%)	e-115

At page 24 please replace Table 1K with the following:

Table 1K. ClustalW Analysis of NOV1

- 1) Novel NOV1a (SEQ ID NO:2)
- 2) Novel NOV1b (SEQ ID NO:4)
- 3) Novel NOV1c (SEQ ID NO:6)
- 4) Novel NOV1d (SEQ ID NO:8)
- 4) ~~gi|13569928|ref|NP-112217.1|~~ gi|13569928| NP 112217 a disintegrin-like and metalloprotease with thrombospondin type 1 motif, 12 [Homo sapiens] (SEQ ID NO:30)
- 5) ~~gi|11493589|gb|AAG35563.1|AF163762.1|~~ gi|11493589| AAG35563 (AF163762) zinc metalloendopeptidase [Homo sapiens] (SEQ ID NO:31)
- 6) ~~gi|10645199|ref|NP-055087.1|~~ gi|10645199| NP 055087 a disintegrin and metalloprotease with thrombospondin motifs-7 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 [Homo sapiens] (SEQ ID NO:32)
- 7) ~~gi|15309931|ref|XP-054419.1|~~ gi|15309931| XP 054419 a disintegrin-like and metalloprotease domain with thrombospondin type I repeats 10 [Homo sapiens] (SEQ ID NO:33)
- 8) ~~gi|7656869|ref|NP-055088.1|~~ gi|7656869| NP 055088 a disintegrin and metalloprotease with thrombospondin motifs-6 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 6 [Homo sapiens] (SEQ ID NO:34)

Applicants: Guo
U.S.S.N.: 09/981,151

```

      10      20      30      40
.....|.....|.....|.....|.....|.....|
NOV1a  MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
NOV1b  MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
NOV1c  -----
NOV1d  MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
gi | 13569928 | -----
gi | 11493589 | -----
gi | 10645199 | -----
gi | 15309931 | -----
gi | 7656869 | -----

```

```

      50      60      70      80
.....|.....|.....|.....|.....|.....|
NOV1a  LEASPPRLLSRGPRRLTAMSPLFSAGTCVRHGTRSGSAWE
NOV1b  LEASPPRLLSRGPRRLTAMSPLFSAGTCVRHGTRSGSAWE
NOV1c  -----MGP---AAAAP-----GSPSV
NOV1d  LEASPPRLLSRGPRRLTAMSPLFSAGTCVRHGTRSGSAWE
gi | 13569928 | ---MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRF
gi | 11493589 | -----
gi | 10645199 | ---MPGGPSPRSPAPLLRPLLLLLLALAPG-APGPAPGRA
gi | 15309931 | -----
gi | 7656869 | -----MEILWKTLTWILSLIMASSEFHS DHRL

```

```

      90      100      110      120
.....|.....|.....|.....|.....|.....|
NOV1a  PERPASSSTRGAAGLDGKGRDMDEAGNERSQQTNTGTENQ
NOV1b  PERPASSSTRGAAGLDGKGRDMDEAGNERSQQTNTGTENQ
NOV1c  PRPPP-----
NOV1d  PERPASSSTRGAAGLDGKGRDMDEAGNERSQQTNTGTENQ
gi | 13569928 | PDRRQEHFIKGL-----
gi | 11493589 | --RSQDEFLSSL-----
gi | 10645199 | TEGR-----
gi | 15309931 | -----
gi | 7656869 | SYSSQEEFLTYL-----

```

```

      130      140      150      160
.....|.....|.....|.....|.....|.....|
NOV1a  TLHVLT-QYDLEVSAYEVDHRGDYVSHETMHHOR-RRRAVA
NOV1b  TLHVLTREYDLEVSAYEVDHRGDYVSHETMHHOR-RRRAVA
NOV1c  -----DLEVSAYEVDHRGDYVSHETMHHOR-RRRAVA
NOV1d  TLHVLT-QYDLEVSAYEVDHRGDYVSHETMHHOR-RRRAVA
gi | 13569928 | -----PEYHVVGFPVRVDASCHETSYGHYPITSSRRKRD
gi | 11493589 | -----ESYETAFPTRVDHNGALAFSPPPP-RRORRG TG
gi | 10645199 | -----AALDTVHPVRVDAGGSFESYELWP--R-ALRKRD
gi | 15309931 | -----
gi | 7656869 | -----EHYQLTIPIRVDQNGAETLSFTVKND-KHSRRRRS

```

```

      170      180      190      200
.....|.....|.....|.....|.....|.....|
NOV1a  VS-----EVES-EHLRIKGRHDFHMDLRTSSSLVAPGFI
NOV1b  VS-----EVES-EHLRIKGRHDFHMDLRTSSSLVAPGFI
NOV1c  VS-----EVEP-AFLOVCRARELRRLCVEAFPIANSQPGFI
NOV1d  VS-----EVES-EHLRIKGRHDFHMDLRTSSSLVAPGFI
gi | 13569928 | ED-----GSEDW-VYYRISHEEKDLFFNLTVNQGFLSNSYI
gi | 11493589 | AT-----AESRLFYKVASPSTHFLNLTTRSSRLLAGHVS
gi | 10645199 | VS-----VRRDAPAFYELOYRGRELRFNLTAHQHLLAPGEV
gi | 15309931 | -----
gi | 7656869 | MDPIDPQQAVSKIFFKLSAYGKHFLNLTLDFTFUSKHET

```

```

      210      220      230      240
.....|.....|.....|.....|.....|.....|

```

Applicants: Guo
U.S.S.N.: 09/981,151

```
NOV1a VQTLGKTGTSVQTLTP--P-EDFCFYQGSLSRSHRNSPSHG
NOV1b VQTLGKTGTSVQTLTP--P-EDFCFYQGSLSRSHRNSPSHG
NOV1c NLSNVRSHWREQHASKRII-TNAMLGESALASTRKS---N
NOV1d VQTLGKTGTSVQTLTP--P-EDFCFYQGSLSRSHRNSPSHG
gi | 13569928 | MEKR-YGNLSHVMMAS--SAPLCHLSGTVLQOGTRVGTA
gi | 11493589 | MEYWTREGLAWQRAARP-----HCLYAGHLQGOASS-SHV
gi | 10645199 | SETRRRGGLGRAHIRAH---TPACHLLGEVODPELEGGLA
gi | 15309931 | -----
gi | 7656869 | MEYWGKDGPOWKHDFLD-----NCHYTCYLQDQRSIT-KV
```

```

250 260 270 280
....|....|....|....|....|....|....|....|
NOV1a GKFCGSTRTLKLCNSQKCPRDSVDERAAQCAEHNSRRFR
NOV1b GKFCGSTRTLKLCNSQKCPRDSVDERAAQCAEHNSRRFR
NOV1c CVFFL-S---FYFFQSGMIRTEADYFLRPLPSHLSWKLG
NOV1d GKFCGSTRTLKLCNSQKCPRDSVDERAAQCAEHNSRRFR
gi | 13569928 | ALSACHG-----LTGFFQLPHGDEFIEPVKKHPLVEG-
gi | 11493589 | AISTCGG-----LHGLIVADEEYFLIEPLHGGPKGS--
gi | 10645199 | AISACDG-----LKGVFQLSNEDYFIEPLDSAPARPG-
gi | 15309931 | -----
gi | 7656869 | ALSNCVG-----LHGVIADEEYFIEPLKNTTDSKH
```

```

290 300 310 320
....|....|....|....|....|....|....|....|
NOV1a GRHYKWKPYTQVEKDLCKLYCTAEGFDFFFSLSNKVKDGT
NOV1b GRHYKWKPYTQVEKDLCKLYCTAEGFDFFFSLSNKVKDGT
NOV1c RAAQGSSPSHVLYKREVLVTSRTWELAHQPLHSSDLRLGL
NOV1d GRHYKWKPYTQVEADLCKLYCTAEGFDFFFSLSNKVKDGT
gi | 13569928 | ----GYEPEIVYRRQKVP-----ETKEP-TCGLKDSV
gi | 11493589 | RSPESGPHVVYKRSSLRHPHLDTACGV-RDEKPKWGRPW
gi | 10645199 | ----HAQPHVVYKROAPER--LAQRGDSSAPSTCGVQVYP
gi | 15309931 | -----
gi | 7656869 | FSYENGHPEHVIYKKSALQQRHLYDHSCHGVSDFTRSKGPW
```

```

330 340 350 360
....|....|....|....|....|....|....|....|
NOV1a PCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
NOV1b PCSEDSRNVCIDGICE-----MPQPPKEDLFILPDE
NOV1c PQKHFCGRRKK-----YMPQPPKEDLFILPDE
NOV1d PCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
gi | 13569928 | NISQ-----KQELWREK
gi | 11493589 | WLRT-----LKPPPAPR
gi | 10645199 | ELES-----RRERWEQR
gi | 15309931 | -----
gi | 7656869 | WLN-----DTSTVSYS
```

```

370 380 390 400
....|....|....|....|....|....|....|....|
NOV1a YKSLRHKRSLLRSHRNEELNVETLVVVDKMMONHGHEN
NOV1b YKSLRHKRSLLRSHRNEELNVETLVVVDKMMONHGHEN
NOV1c YKSLRHKRSLLRSHRNEELNVETLVVVDKMMONHGHEN
NOV1d YKSLRHKRSLLRSHRNEELNVETLVVVDKMMONHGHEN
gi | 13569928 | WERHNLPSRSLSRSSISKERWVETLVVADTKMEYHGSSE
gi | 11493589 | LGNETERGQPLKRSVSRERYVETLVVADKMMVAYHGRRD
gi | 10645199 | QDWRPRLRLRLRQSVSRERWVETLVVADAKMVEYHGOPO
gi | 15309931 | -----MMVAYHGRRD
gi | 7656869 | LPINNTHIHRQKRSVSIERFVETLVVADKMMVGYHGRGD
```

```

410 420 430 440
....|....|....|....|....|....|....|....|
NOV1a ITTYVLTIEINMVSALFKDGTIGG-----NINIAIVGLILL
NOV1b ITTYVLTIEINMVSALFKDGTIGG-----NINIAIVGLILL
NOV1c ITTYVLTIEINMVSALFKDGTIGG-----NINIAIVGLILL
NOV1d ITTYVLTIEINMVSALFKDGLMCKDGTTRHDHAILTGLDTC
```

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi | 13569928 | VESYILTINMVTGLFHNPSIGN-----ATHIVMVRLLIL  
gi | 11493589 | VEQYVLAIMNIVAKLFODSSIGS-----TVNILVTRLILL  
gi | 10645199 | VESYVLTINMVTGLFHNPSIGN-----PTHTITVRLVLL  
gi | 15309931 | VEQYVLAIMNIVAKLFODSSIGS-----TVNILVTRLILL  
gi | 7656869 | TEHYILSVMNIVAKLYRDSISGN-----VNIIIVARLIVL
```

```
450 460 470 480  
NOV1a EDEQPGLVISHHADHTLS SFCQWQSGIMGKDG-----  
NOV1b EDEQ-----  
NOV1c EDEQPGLVISHHADHTLS SFCQWQSGIMGKDG-----  
NOV1d SWKN-----  
gi | 13569928 | EEEQGLKIVVHHAERTLS SFCQWQKSINPKS-----DL  
gi | 11493589 | TEDOPTLEITHHAGKSLD SFCQWQKSIIVNHSGHGNAIPEN  
gi | 10645199 | EDEEEDLKITHHADNTEK SFCQWQKSINMKG-----DA  
gi | 15309931 | TEDOPTLEITHHAGKSLD SFCQWQKSIIVNHSGHGNAIPEN  
gi | 7656869 | TEDQPNLEINHHAOKSLD SFCQWQKSHLSHQSDGNTIPEN
```

```
490 500 510 520  
NOV1a --TRHDEAILLTGLDICSWKNEPCDTLGFAPISGMCSKYR  
NOV1b -----  
NOV1c --TRHDEAILLTGLDICSWKNEPCDTLGFAPISGMCSKYR  
NOV1d -----PCDTLGFAPISGMCSKYR  
gi | 13569928 | NPVHHDVAVLLTRKDICAGFNRPCEITGLSHLSGMCQPHR  
gi | 11493589 | GVANHDTAVLLTRYDICIYKNKPCGTLGLAPVGGMCERER  
gi | 10645199 | HPLHHDVAVLLTRKDICAMNRPCEITGLSHVAGMCQPHR  
gi | 15309931 | GVANHDTAVLLTRYDICIYKNKPCGTLGLAPVGGMCERER  
gi | 7656869 | GIAHHDNAVLLTRYDICTYKNKPCGTLGLASVAGMCERER
```

```
530 540 550 560  
NOV1a SCINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEG  
NOV1b -----  
NOV1c SCINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEG  
NOV1d SCINEDTGLGLAFTIAHESGHNFGMIHDGEGNMCKKSEG  
gi | 13569928 | SCINEDSGLPLAFTIAHELGHSEGLQHDGKENDCEPVGR  
gi | 11493589 | SCSVNEDIGLPLAFTIAHEIGHTFGMNHGCVGNSCGARGQ  
gi | 10645199 | SCSINEDTGLPLAFTVAHELGHSEGLQHDGSGNDCEPVGK  
gi | 15309931 | SCSVNEDIGLATAFTIAHEIGHTFGMNHGCVGNSCGARGQ  
gi | 7656869 | SCSINEDIGLGSFTIAHEIVHNEGMNHGCI GNSCGRK--
```

```
570 580 590 600  
NOV1a N---DMSPTLAGNGVSWSPCSROYLHKFLSTAQAICLA  
NOV1b -----  
NOV1c N---DMSPTLAGNGVSWSPCSROYLHKFLSTAQAICLA  
NOV1d N---DMSPTLAGNGVSWSPCSROYLHKFLSTAQAICLA  
gi | 13569928 | HP-YHMSRQIQYDPTPLTWSKCSEEVITRELDRGWGFCID  
gi | 11493589 | DPAKMAAHITMTNPVWSSCSRDYITSELD SGLGLCLN  
gi | 10645199 | RP-FHMSPOLLYDAAPLTWSRCSROYITRELDRGWGFCID  
gi | 15309931 | DPAKMAAHITMTNPVWSSCSRDYITSELD SGLGLCLN  
gi | 7656869 | -----VMKQONYG-SSHYCEYQSFE-----VCLQ
```

```
610 620 630 640  
NOV1a DQPKPVKEYKYPEKLPGE LYDANTOCKWOFGEKAKLCMLD  
NOV1b -----  
NOV1c DQPKPVKEYKYPEKLPGE LYDANTOCKWOFGEKAKLCMLD  
NOV1d DQPKPVKEYKYPEKLPGE LYDANTOCKWOFGEKAKLCMLD  
gi | 13569928 | DIPKK-KGLSKSVIAPGVINDVHHQCOLQYG--PNATFCQ  
gi | 11493589 | NRPPR-QDFVYPTVAPGOAYDADEQCRFOH---GVKSRQC  
gi | 10645199 | DPPAK-DIIDEPSVPPGVLYDVSHQCRLOYG--AYSACE  
gi | 15309931 | NRPPR-QDFVYPTVAPGOAYDADEQCRFOH---GVKSRQC
```

Applicants: Guo
U.S.S.N.: 09/981,151

gi|7656869| SRX-----HHQ

```

      650      660      670      680
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a  FKKDICKALWCHRIGRKCE TKFMPAAEGTICG----HDMW
NOV1b  ---DICKALWCHRIGRKCE TKFMPAAEGTICG----HDMW
NOV1c  FKKDICKALWCHRIGRKCE TKFMPAAEGTICG----HEHG
NOV1d  FKKDICKALWCHRIGRKCE TKFMPAAEGTICG----HDMW
gi|13569928| EVENVCOTLWCSVKG-FCRSKLDAAADGTCCG----EKKW
gi|11493589| KYGEVCSSELWCLSKSNRCITNSIPAAEGTICOTHTIDKGW
gi|10645199| DMDNVCHTLWCSVGT-TCHSKLDAAVDGTCCG----ENKW
gi|15309931| KYGEVCSSELWCLSKSNRCITNSIPAAEGTICOTHTIDKGW
gi|7656869| LFRVVCSELWCLSKSNRCITNSIPAAEGTICOTGNIEKGW
```

```

      690      700      710      720
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a  CRGGCCVKYGDDEGPKPTHGHWSDWSSWSPCSRTC GGGVSH
NOV1b  CRGGCCVKYGDDEGPKPTHGHWSDWSSWSPCSRTC GGGVSH
NOV1c  A-GGCVKYGDDEGPKPTHGHWSDWSSWSPCSRTC GGGVSH
NOV1d  CRGGCCVKYGDDEGPKPTHGHWSDWSSWSPCSRTC GGGVSH
gi|13569928| CMAGKCLTVGKK-PE SIPPGGWGRWSPWSECSRTC GAGVQS
gi|11493589| CYKRVCPVPGSR-PEGVDGAWGPWLPWGD CSRTC GGGVSS
gi|10645199| CLSGECVPVGFPR-PEAVDGGWSGWSAWSICSRSCGMGVQS
gi|15309931| CYKRVCPVPGSR-PEGVDGAWGPWLPWGD CSRTC GGGVSS
gi|7656869| CYQGD CVPVGTW-PSIDGGWGPWSLWGECSRTC GGGVSS
```

```

      730      740      750      760
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a  RSR-LCTNPNPSEGGKECEGSTRTLKLCNSQKCPRDSVDF
NOV1b  RSR-LCTNPRPSEGGKECEGSTRTLKLCNSQKCPRDSVDF
NOV1c  RSRSONTHSRPSEGGKECEGSTRTLKLCNSQKCPRDSVDF
NOV1d  RSR-LCTNPKPSEGGKECEGSTRTLKLCNSQKCPRDSVDF
gi|13569928| AER-LCNNPEPKFGGKYCTGERKRYRLCNVHPCRSEAPTF
gi|11493589| SSR-HCDSPRPPIGGKYCLGERRRHSCNEDDCPPGSQDF
gi|10645199| AER-OCTOPTPKYKGRYCVGERKRFRLCNLQACPAGRPSE
gi|15309931| SSR-HCDSPRPPIGGKYCLGERRRHSCNEDDCPPGSQDF
gi|7656869| SLR-HCDSPAPSGGGKYCLGERKRYSCNEDDCPLGSRDF
```

```

      770      780      790      800
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a  RAAQCAEHNSRRFRGRHYKWKP-----QDLCKLYCTAEG
NOV1b  RAAQCAEHNSRRFRGRHYKWKP-----QDLCKLYCTAEG
NOV1c  RAAQCAEHNSRRFRGRHYKWKP-----DQDLCKLYCTAEG
NOV1d  RAAQCAEHNSRRFRGRHYKWKPYPYQVEDQDLCKLYCTAEG
gi|13569928| ROMQCSEFDIVPYGNELVHWFI FN--PAHPCELYCRPID
gi|11493589| REVQCSEFDSIPFRGKFKWKTYRGG-GVKACSLTSLAEG
gi|10645199| RHVQCSEHFDAMLKGOLETWVPVFN--DVNPCELEHCRPAN
gi|15309931| REVQCSEFDSIPFRGKFKWKTYRGG-GVKACSLTSLAEG
gi|7656869| REKQCAQFDNMPFRGKYFNWKPYTGG-GVKPCALNCLAEG
```

```

      810      820      830      840
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a  FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICEX-GCDNV
NOV1b  FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICE--GCDNV
NOV1c  FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICERVGCDNV
NOV1d  FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICERVGCDNV
gi|13569928| GQFSEKMLDAVIDGTPCFEGGNSRNVCINGICKMVGCDYE
gi|11493589| ENFYTERAAAVVDGTPCR--PDIVDTCVSGECKRHVGCDRV
gi|10645199| EYFAKTERDAVVDGTPCYQVRASRDICINGICKNVGCDFE
gi|15309931| ENFYTERAAAVVDGTPCR--PDIVDTCVSGECKRHVGCDRV
gi|7656869| ENFYTERAPAVIDGTQCN--ADSLDTCINGECKRHVGCDNI
```

```

      850      860      870      880
.....|.....|.....|.....|.....|.....|.....|.....|
```


Applicants: Guo
U.S.S.N.: 09/981,151

```
NOV1a LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTN-HYHNV
NOV1b LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTN-VYHNV
NOV1c LGSDAVEDVCGVCNGNNSACTIHRGLY---LE---VYHNV
NOV1d LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYHNV
gi | 13569928 | HDSNATEDRCGVCLGSGSCQTVRKMEKQKE-GSGYVDIG
gi | 11493589 | LGSDLREDKCRVCGGSGSACETIEGVSPASPGAGYEDVV
gi | 10645199 | HDSGAMEDRCGVCHGNGSTCHTVSGTEEEAE-GLGYVDVG
gi | 15309931 | LGSDLREDKCRVCGGSGSACETIEGVSPASPGAGYEDVV
gi | 7656869 | LGSDAREDRCRVCGGGSTCDAIEGFTNDLSLPRGGYMEVV
```

```
890 900 910 920
NOV1a TIPSGARSIRIYEMNVSTSYTSVRN-ALRRYYLNGHWTV
NOV1b TIPSGARSIRIYEMNVSTSYTSVRN-ALRRYYLNGHWTV
NOV1c TIPSGARSIRIYEMNVSTSYTSVRN-ALRRYYLNGHWTV
NOV1d TIPSGARSIRIYEMNVSTSYTSVRN-ALRRYYLNGHWTV
gi | 13569928 | LIPKGARDIRVMEIEGAGNEFAIRSEDPEKYVYLNCGEIIQ
gi | 11493589 | WIPKCSVHIFIODENLSLSEALAKGDQ-ESLLLEGLPGTP
gi | 10645199 | LIPAGAREIRIQEVAEAAEFAIRSEDPEKYVYLNCGEIIQ
gi | 15309931 | WIPKCSVHIFIODENLSLSEALAKGDQ-ESLLLEGLPGTP
gi | 7656869 | QIPKCSVHIEVREVAESKNYIAIRSEG-DDYYLNGAWTID
```

```
930 940 950 960
NOV1a WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVELLF
NOV1b WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVELLF
NOV1c WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVELLF
NOV1d WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVELLF
gi | 13569928 | WNGNYKLAGTVEQYDRKGD-LEKLMATGPTNESVWVQLLF
gi | 11493589 | QPHRLPLAGTTFQLRQGPQVQSLEALGPINASTLIVMVL
gi | 10645199 | WNGDYQVAGTTFYARRGN-WENLTSPGPTKEPVWVQLF
gi | 15309931 | QPHRLPLAGTTFQLRQGPQVQSLEALGPINASTLIVMVL
gi | 7656869 | WPRKEDVAGTAEHYKRPTEPESEALGPTSENLIIVMVL
```

```
970 980 990 1000
NOV1a QGRNPGVAWEYS-----
NOV1b QGRNPGVAWEYS-----
NOV1c QGRNPGVAWEYS-----
NOV1d QGRNPGVAWEYS-----
gi | 13569928 | QVTNPGIKYEYTIQKDGLDNDVEQMYFWQYGHWTECSVTC
gi | 11493589 | RTELPAIRYREN-----
gi | 10645199 | -----
gi | 15309931 | RTELPAIRYREN-----
gi | 7656869 | QEONLGIRYKEN-----
```

```
1010 1020 1030 1040
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | GTGIRRQTAHCIIKGRGMVKATFCDPETQPNRQKKCHEK
gi | 11493589 | -APIAR-----DS
gi | 10645199 | ---VP-----
gi | 15309931 | -APIAR-----DS
gi | 7656869 | -VPITRTGSG-----DN
```

```
1050 1060 1070 1080
NOV1a -----MPRLGTE-----
NOV1b -----MPRLGTE-----
NOV1c -----MPRLGTE-----
NOV1d -----MPRLGTE-----
```


Applicants: Guo
U.S.S.N.: 09/981,151

gi|13569928| ACPPRWWAGEWEACSATCGPHGEKKRTVLCIQTMVSDEQA
gi|11493589| LPPYSWHYAPWTKCSAQAGGSQV-QAVECRNQL--DSSA
gi|10645199| -----ASRCPPGGGS-R-----GG
gi|15309931| LPPYSWHYAPWTKCSAQAGGSQV-QAVECRNQL--DSSA
gi|7656869| EVGFTWNHQPWSECSATCAGG-----

1090 1100 1110 1120
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a -----KOPPAOP-----
NOV1b -----KOPPAOP-----
NOV1c -----KOPPAOPS-----
NOV1d -----KOPPAOPS-----
gi|13569928| LPPTDCQ-HLLKPKTLLSCNRDILCPDWTGVGNWSECSVS
gi|11493589| VAPHYCSAHSKLPKRQACNTEP-CPPDWVVGWNSLCSRS
gi|10645199| VP-----RPSTLHGRSR-----P---
gi|15309931| VAPHYCSAHSKLPKRQACNTEP-CPPDWVVGWNSLCSRS
gi|7656869| -----KMPTRQ-----P-----TQR

1130 1140 1150 1160
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a -----YTWATVR-----
NOV1b -----YTWATVR-----
NOV1c -----YTWATVR-----
NOV1d -----YTWATVR-----
gi|13569928| CGGGVRIKSVTCAKNHDEPCDVTRKPNRSLCGLQCCPSS
gi|11493589| CDAGVRERSVVCQR-----
gi|10645199| --GGVSPGKSVT-----E-PGS-----
gi|15309931| CDAGVRERSVVCQR-----
gi|7656869| --ARWRKHHLSY-----

1170 1180 1190 1200
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi|13569928| RRVLPKNKGTISNGKNPPTLKPVPPTSRPRMLTTPTGPE
gi|11493589| -----RVSAAEKALDDSACPQ-----
gi|10645199| -----EPGPPAAAS-----
gi|15309931| -----RVSAAEKALDDSACPQ-----
gi|7656869| -----ALCLLKKLIGNISCR-----

1210 1220 1230 1240
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a -----SECSVSCGGGRC
NOV1b -----SECSVSCGGGRC
NOV1c -----SECSVSCGGGRC
NOV1d -----SECSVSCGGGRC
gi|13569928| SMSTSTPAISSPSPTTASKEGDLGGKQWODS--STQPELS
gi|11493589| ---PRPPVLEACHGPTCPPEW--AALDWSECTPSCGPGLR
gi|10645199| -T-SVSPSLKWPNLVAAVHRG-----GWGQA--PLGLGGW
gi|15309931| ---PRPPVLEACHGPTCPPEW--AALDWSECTPSCGPGLR
gi|7656869| -----FAS--SCN--LA

1250 1260 1270 1280
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a LPVLLLEACQPSATAYIALAFLES-----
NOV1b LPVLLLEACQPSATAYIALAFLES-----
NOV1c LPVLLLEACQPLATAYIALAFLES-----
NOV1d LPVLLLEACQPSATAYIALAFLES-----
gi|13569928| SRYLSTGSTSQPILTQSLSIQPSEENVSSSDTGPTSEG
gi|11493589| HRVVLCKSADHRATLPPAHCSPAAKP-----
gi|10645199| RRHLVLMG---PRLPTQLLFQE-----SNP
gi|15309931| HRVVLCKSADHRATLPPAHCSPAAKP-----

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi|7656869| KETL-----
                1290      1300      1310      1320
                ....|....|....|....|....|....|....|
NOV1a          -----
NOV1b          -----
NOV1c          -----
NOV1d          -----
gi|13569928| GLVATTTSGSGLSSSRNPITWPVTPFYNTLTGPEMEIHS
gi|11493589| -----PAT
gi|10645199| G-----VHYEYT-----IHR
gi|15309931| -----PAT
gi|7656869| -----
                1330      1340      1350      1360
                ....|....|....|....|....|....|....|
NOV1a          -----
NOV1b          -----
NOV1c          -----
NOV1d          -----
gi|13569928| GSGEEREQPEDKDESNPVIWTKIRVPGNDAPVESTEMPLA
gi|11493589| MRCNLRRCPP-----
gi|10645199| EAGGHDEVPP-----
gi|15309931| MRCNLRRCPP-----
gi|7656869| -----
                1370      1380      1390      1400
                ....|....|....|....|....|....|....|
NOV1a          -----
NOV1b          -----
NOV1c          -----
NOV1d          -----
gi|13569928| PPLTPDLSRESWWPPFSTVMEGLLPSQRPTTSETGTPRVE
gi|11493589| -----
gi|10645199| -----
gi|15309931| -----
gi|7656869| -----
                1410      1420      1430      1440
                ....|....|....|....|....|....|....|
NOV1a          -----
NOV1b          -----
NOV1c          -----
NOV1d          -----
gi|13569928| GMVTEKPANTLLPLGGDHQPEPSGKTANRNHLKLPNNMNQ
gi|11493589| -----
gi|10645199| -----
gi|15309931| -----
gi|7656869| -----
                1450      1460      1470      1480
                ....|....|....|....|....|....|....|
NOV1a          -----
NOV1b          -----
NOV1c          -----
NOV1d          -----
gi|13569928| TKSSSEPVLTEEDATSLITEGFLLNASNYKQLTNGHGSAAHW
gi|11493589| -----ARW
gi|10645199| -----PVFS-----W
gi|15309931| -----ARW
gi|7656869| -----
                1490      1500      1510      1520
                ....|....|....|....|....|....|....|
```

Applicants: Guo
U.S.S.N.: 09/981,151

NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | IVGNWSECSTTCGLGAYWKRVECTTQMDSDCAAIQRPDPA
gi | 11493589 | VAGEWGECSAQCGVGQRQRSVRCTS-----
gi | 10645199 | HYGPWTKCTVTCGRGE-----
gi | 15309931 | VAGEWGECSAQCGVGQRQRSVRCTS-----
gi | 7656869 | -----

1530 1540 1550 1560
....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | KRCHLRPCAGWKVGNWSKCSRNCSSGGFKIREIQCVDSRDH
gi | 11493589 | -----HTGQASHECTEALR-----
gi | 10645199 | -----KWGRHSPTCRG-----LVSGQGH
gi | 15309931 | -----HTGQASHECTEALR-----
gi | 7656869 | -----

1570 1580 1590 1600
....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | RNLRPFHCQFLAGIPPPLSMSCNPEPCEAWQVEPWSQCSR
gi | 11493589 | -----PPTTQQCEA
gi | 10645199 | -----WLQLPA
gi | 15309931 | -----PPTTQQCEA
gi | 7656869 | -----

1610 1620 1630 1640
....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | SCGGGVQERGVFCPGLCDWTKRPTSTMSCNEHLCCHWAT
gi | 11493589 | KCDS-----PTPG
gi | 10645199 | HC-----WAT
gi | 15309931 | KCDS-----PTPG
gi | 7656869 | -----

1650 1660 1670 1680
....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | GNWDLCTSCGGGFQKRIVQCVPSSEGNKTEDQDQCLCDHK
gi | 11493589 | DGPEECKDVN-----
gi | 10645199 | TGLEVCFS-----E-----
gi | 15309931 | DGPEECKDVN-----
gi | 7656869 | -----

1690 1700 1710 1720
....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----

Applicants: Guo
U.S.S.N.: 09/981,151

gi 13569928	PRPPEFKKCNQQACKKSADLLCTKDKLSASFCQTLKAMKK	
gi 11493589	-----KVAYCPLVLKFQF	
gi 10645199	---P-----QF-----S-ICEMRLAIAL	
gi 15309931	-----KVAYCPLVLKFQF	
gi 7656869	-----	

	1730	1740	1750	
			
NOV1a	-----			(SEQ ID NO:2)
NOV1b	-----			(SEQ ID NO:4)
NOV1c	-----			(SEQ ID NO:6)
NOV1d	-----			(SEQ ID NO:8)
gi 13569928	CSVPTVRAECCFSCPQTHITHTQRRQRLQKSKEL			(SEQ ID NO:30)
gi 11493589	CSRAYFRQMCCCKTCQGH-----			(SEQ ID NO:31)
gi 10645199	CPRPAGRVHG-----			(SEQ ID NO:32)
gi 15309931	CSRAYFRQMCCCKTCHGH-----			(SEQ ID NO:33)
gi 7656869	-----			(SEQ ID NO:34)

At page 32, please replace paragraph at lines 31-42 with the following new paragraph:

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the European Bioinformatics Institute Interpro. website (~~http://www.ebi.ac.uk/interpro~~). DOMAIN results for NOV1 as disclosed in Tables 1L-IO, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Table 1E and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (|) and “strong” semi-conserved residues are indicated by grey shading or by the sign (+). The “strong” group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK (SEQ ID NO: 161), NHQK (SEQ ID NO: 162), NDEQ (SEQ ID NO: 163), QHRK (SEQ ID NO: 164), MILV (SEQ ID NO: 165), MILF (SEQ ID NO: 166), HY, FYW.

At page 33, please replace Table 1L with the following:

Table 1L. Domain Analysis of NOV1	
gnl Pfam pfam01421, Reprolysin, Reprolysin (M12B) family zinc metalloprotease. The members of this family are enzymes that cleave peptides. These proteases require zinc for catalysis. Members of this family are also known as adamalysins. Most members of this family are snake venom endopeptidases, but there are also some mammalian proteins, and fertilin. Fertilin and closely related proteins appear to not have some active site residues and may not be active enzymes. (SEQ ID NO:76)	
CD-Length = 199 residues, 95.0% aligned	
Score = 122 bits (307), Expect = 7e-29	

Query:	378	DKKMMQNHG--HENITTYVLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPGLVISH	435
		+ + + + + + + +	
Sbjct:	10	DHGMFTKYGSDLNKIRQRVHQIVNLVNEIYRPL---NIRVVLVGLIWSGDGK-ITVQG	64
Query:	436	HADHTLSSFCQWQSGLMGKDGRHDHAILLTGLDICSWKNEPCDTLGFAPISGMCSKYRS	495
		+ + + + + + + + + + + +	
Sbjct:	65	DANDTLHRFLEWRETDLLKR-KSHDNAQLLTGIDF-----DGNTIGAAYVGGMCSPKRS	117
Query:	496	CTINED---TGLGLAFTIAHESGHNFGMIHDGEGN-MCKKSEGNIMSPTLAGRNGVFSWS	551
		+ + + + + + + + + + + + +	
Sbjct:	118	VGTVQDHSPIVLLVAVTMAHELGHNLGMTHDDINKCTCEGGGGCIMPVASSSPGKK-FS	176
Query:	552	PCSRQYLHKFLSTAQAICLADQ	573 (aa 378-573 of SEQ ID NO:2)
		+ + + + + + + + + + +	
Sbjct:	177	NCSMDDYQQFLTKGKPQCLLNK	198 (SEQ ID NO:76)

At page 33, please replace Table 1M with the following:

Table 1M. Domain Analysis of NOV1	
gnl Smart smart00209, TSP1, Thrombospondin type 1 repeats; Type 1 repeats in thrombospondin-1 bind and activate TGF-beta. (SEQ ID NO:77)	
CD-Length = 51 residues, 100.0% aligned	
Score = 63.5 bits (153), Expect = 5e-11	

Query:	668	WSDWSSWSPCSRTCAGGVSHRSLCTNPNP SHGGKFCEGSTRTLKLCNSQKCP	720 (of SEQ ID NO:2)
		+ + +	
Sbjct:	1	WGEWSEWSPCSVTCAGGVQTRTRCCNPPN--GGGPCTGPDTETRACNEQPCP	51 (SEQ ID NO:77)

At page 33, please replace Table 1N with the following:

Applicants: Guo
U.S.S.N.: 09/981,151

Table 1N. Domain Analysis of NOV1

~~gnl|Pfam|pfam00090~~, tsp_1, Thrombospondin type 1 domain. (SEQ ID NO:78)
CD-Length = 48 residues, 100.0% aligned
Score = 54.7 bits (130), Expect = 2e-08

Query: 669 SDWSSWSPCSRTC GGGVSHRSLCTNP NPSHGGKFCEGSTR TLKLCNSQKC 719 (of SEQ ID NO:2)
| | | | | | | | | + | | | + | | | | | + + |
Sbjct: 1 SPWSEWSPCSVTCGKGIRTRQRTCNSP---AGGKPCTGDAQETEACMMMDPC 48 (SEQ ID NO:78)

At page 34, please replace Table 1O with the following:

Table 1O. Domain Analysis of NOV1

~~gnl|Pfam|pfam01562~~, Pep_M12B_propep, Reprolysin family propeptide.
This region is the propeptide for members of peptidase family M12B.
The propeptide contains a sequence motif similar to the "cysteine switch" of the matrixins. This motif is found at the C terminus of the alignment but is not well aligned. repeats. (SEQ ID NO:79)
CD-Length = 117 residues, only 39.3% aligned
Score = 38.5 bits (88), Expect = 0.002

Query: 180 LRTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGS LRSHRNS 225 (of SEQ ID NO:2)
| + ||+|| | | | | | + + | +||| + + ||
Sbjct: 2 LEKNRSL LAPDFTVTYDDGTLVTEHPLIQDHCYYQGYVEGY PNS 47 (SEQ ID NO:79)

At page 41 please replace Table 2C with the following:

Table 2C. BLAST results for NOV2

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 14765710 ref XP_006925.4 XP 006925	alpha 2 macroglobulin precursor [Homo sapiens]	1474	593/1486 (39%)	870/1486 (57%)	0.0
gi 4557225 ref NP_000005.1 NP 000005	alpha 2 macroglobulin precursor [Homo sapiens]	1474	591/1486 (39%)	869/1486 (57%)	0.0
gi 224053 prf 1009174A 1009174A	macroglobulin alpha2 [Homo sapiens]	1450	585/1471 (39%)	861/1471 (57%)	0.0

Applicants: Guo
U.S.S.N.: 09/981,151

<u>gi</u> <u>6978425</u> <u>ref</u> <u>NP 036620.1</u> <u>NP 036620</u>	alpha-2-macroglobulin [Rattus norvegicus]	1472	578/1483 (38%)	867/1483 (57%)	0.0
<u>gi</u> <u>2144118</u> <u>pir</u> <u>JC5143</u> <u>JC5143</u>	alpha-macroglobulin precursor - guinea pig	1476	570/1495 (38%)	858/1495 (57%)	0.0

At page 41 please replace Table 2D with the following:

Table 2D. ClustalW Analysis of NOV2

- 1) NOV2 (SEQ ID NO:10)
2) gi|14765710|ref|XP_006925.4| gi|14765710| XP_006925 alpha 2 macroglobulin precursor [Homo sapiens] (SEQ ID NO:35)
2) gi|4557225|ref|NP_000005.1| gi|4557225| NP_000005 alpha 2 macroglobulin precursor [Homo sapiens] (SEQ ID NO:36)
3) gi|224053|prf|1009174A gi|224053| 1009174A macroglobulin alpha2 [Homo sapiens] (SEQ ID NO:37)
4) gi|6978425|ref|NP_036620.1| gi|6978425| NP_036620 alpha-2-macroglobulin [Rattus norvegicus] (SEQ ID NO:38)
5) gi|2144118|pir|JC5143 gi|2144118| JC5143 alpha-macroglobulin precursor - guinea pig (SEQ ID NO:39)

570 580 590 600

NOV2
gi | 14765710 | SLVIYAILPSPGCVADKIQESVEMCFDN-----QQL
gi | 4557225 | RLLIYAVLPAGDVIGDSAKYDVENCLANKVDLSFSPSQSL
gi | 224053 | RLLIYAVLPAGDVIGDSAKYDVENCLANKVDLSFSPSQSL
gi | 6978425 | RLVIYAALPNGEVVGDIAKYIEINCLANKVDLVFRPN SGL
gi | 2144118 | RLLIYAILPSGTIIADS AKYN VENC LDKVNLS FSEGQS L

610 620 630 640
 | | |
 NOV2 PGAEVLELOLOAAPGSPCALRAVDLSVLLLRPPDRELSNRSV
 gi | 14765710 | PASEAHLRVTAAPQSVCALRAVDQSVLLMKPDAELSASSV
 gi | 4557225 | PASEAHLRVTAAPQSVCALRAVDQSVLLMKPDAELSASSV
 gi | 224053 | PASEAHLRVTAAPQSVCALRAVDQSVLLMKPDAELSASSV
 gi | 6978425 | PAIRALLSVMASPOSTCGGLRAVDQSVLLMKPDELTELASLLE
 gi | 2144118 | PASKTHLRVTASPOSTCALRAVDQSVLLLRKPEAVLSASSV

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....
650 660 670 680

NOV2 YGMFP-FWYGHYPYQVAEYDQCVPVSGPWDFPQPLIDPMPO
gi | 14765710 | YNLLPEKDLTGFPGLNDQDNED-----CENR
gi | 4557225 | YNLLPEKDLTGFPGLNDQDDED-----CENR
gi | 224053 | YNLLPEKDLTGFPGLNDQDDED-----CENR
gi | 6978425 | YDLLPVKDLTGFPQGADQREEDING-----CVKG
gi | 2144118 | YALLPVKDLTGFPGLLGQQEENDGE-----CVSL

690 700 710 720

 NOV2 G E S S Q R S I I R P S F S E G - T D L S F F R D V G L K I L S N K I R K
 gi | 14765710 | E N V Y I N G I T Y T P V S S T N E K D M Y S F L E D M G L K A F T N S K I R K
 gi | 4557225 | E N V Y I N G I T Y T P V S S T N E K D M Y S F L E D M G L K A F T N S K I R K
 gi | 224053 | E N V Y I N G I T Y T P V S S T N E K D M Y S F L E D M G L K A F T N S K I R K
 gi | 6978425 | N D T Y I N G I L Y S P V N T N E E D M Y G F L R D M G L K V F T N S N I R K
 gi | 2144118 | V N T Y I D G I L Y S P E P N I N E K D M Y G F L R D M G L K V F T N I K I K

Applicants: Guo
U.S.S.N.: 09/981,151

```

      730      740      750      760
      |.....|.....|.....|.....|.....|.....|.....|.....|
NOV2  PVDCSHRSPEYST---AMGGGGHPAFESSTP-----
gi | 14765710 | PKMCPOLQOYEMHGPEGIRVGYESDVMGRGHARLVEHV--
gi | 4557225 | PKMCPOLQOYEMHGPEGIRVGYESDVMGRGHARLVEHV--
gi | 224053 | PKMCPOLQOYEMHGPEGIRVGYESDVMGRGHARLVEHV--
gi | 6978425 | PKVCERLEDNKGIPAAAYHLVSQSHMDAFLE-----
gi | 2144118 | POLCAHVOKTEVP---TMAYSSESSEFRSGPRRYPAVGI

```

```

      770      780      790      800
      |.....|.....|.....|.....|.....|.....|.....|.....|
NOV2  ---LHQARDSQVROYFPETWIWDLFPITGNSGKEAVEVTVP
gi | 14765710 | ---EEPETETVRKYFPETWIWDLVVNSAGVAEVCVTVP
gi | 4557225 | ---EEPETETVRKYFPETWIWDLVVNSAGVAEVCVTVP
gi | 224053 | ---EEPETETVRKYFPETWIWDLVVNSAGVAEVCVTVP
gi | 6978425 | S---SESPETETRRSYFPETWIWDLVVNSAGVAEVCVTVP
gi | 2144118 | AATYSEPPKETVRITYSPETWIWDLKVIDSSGVAEVCVTVP

```

```

      810      820      830      840
      |.....|.....|.....|.....|.....|.....|.....|.....|
NOV2  DAITEWKAMSECLSSSRGFGISPTVGLTAFPEFVDLTTP
gi | 14765710 | DTITWKAQAFCLSEDAGLGISSTASLRAFQPFVELTMP
gi | 4557225 | DTITWKAQAFCLSEDAGLGISSTASLRAFQPFVELTMP
gi | 224053 | DTITWKAQAFCLSEDAGLGISSTASLRAFQPFVELTMP
gi | 6978425 | DTITWKAQAFCLSNDTGLGISPVVQFAFQPFVELTMP
gi | 2144118 | DTITWKAQAFCLSNDTGLGISPASLRAFQPFVELTMP

```

```

      850      860      870      880
      |.....|.....|.....|.....|.....|.....|.....|.....|
NOV2  YSVIRGESFRLTATFNLYLKDCIRVQDLAKSHEYQLESW
gi | 14765710 | YSVIRGEAFTLKATVLNLYLPKCIRVSVQLEASPAFLAVPV
gi | 4557225 | YSVIRGEAFTLKATVLNLYLPKCIRVSVQLEASPAFLAVPV
gi | 224053 | YSVIRGEAFTLKATVLNLYLPKCIRVSVQLEASPAFLAVPV
gi | 6978425 | YSVIRGEAFTLKATVLNLYLPTCIRVSVQLEASPDFLAAPE
gi | 2144118 | YSVIRGEAFTLKATVLNLYLPDCIRVSVHLEASPKFLAEPK

```

```

      890      900      910      920
      |.....|.....|.....|.....|.....|.....|.....|.....|
NOV2  ADSQTSSCIACDDAKTHEWNETAVKLGHEINETISTILDS
gi | 14765710 | EKEQAPHCIICANGROTQVSWAVTPKSLGNVNETVSAEALNS
gi | 4557225 | EKEQAPHCIICANGROTQVSWAVTPKSLGNVNETVSAEALNS
gi | 224053 | EKEQAPHCIICANGROTQVSWAVTPKSLGNVNETVSAEALNS
gi | 6978425 | EKEQASHCICMNRHTASWAVIPKSLGNVNETVSAEALNS
gi | 2144118 | AKEQESYCVCGNEROTQVSWVTPKSLGNVNETVSAEALNS

```

```

      930      940      950      960
      |.....|.....|.....|.....|.....|.....|.....|.....|
NOV2  NEPCGGQKGFVPQKGRSDTPIKPVLVKPEGVLVEKTHSSL
gi | 14765710 | QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi | 4557225 | QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi | 224053 | QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi | 6978425 | RELCGNEVPVPEQGRKDTVIKSLLVEPEGLENEVTFNSL
gi | 2144118 | SELCGNEKTVVPTVGRKDTVIKPLLVEPEGLEKETTFNSL

```

```

      970      980      990     1000
      |.....|.....|.....|.....|.....|.....|.....|.....|
NOV2  LCPKGGKVASSESVSLPLVDIVPESTKAYVVLGDIIGTA
gi | 14765710 | LCPSGGEVS-EELSLKLPPNVVEESARASVSVLGDILGSA
gi | 4557225 | LCPSGGEVS-EELSLKLPPNVVEESARASVSVLGDILGSA
gi | 224053 | LCPSGGEVS-EELSLKLPPNVVEESARASVSVLGDILGSA
gi | 6978425 | LCPMGAEVS-EELSLKLPPNVVEESARASVSVLGDILGSA
gi | 2144118 | IRVSDTTVS-EELSLKLPPNVVEESARASVSVLGDILGSA

```

1010 1020 1030 1040

Applicants: Guo
U.S.S.N.: 09/981,151

NOV2
gi | 14765710 |
gi | 4557225 |
gi | 224053 |
gi | 6978425 |
gi | 2144118 |

.....|.....|.....|.....|.....|.....|.....|.....|
QONLDGLVQMPSCGCEONMVLFAPIIYVLOMLEKAGLLTE
MONTQNLLOMPYGCCEONMVLFAPIYVLDYLNETOQLTP
MONTQNLLOMPYGCCEONMVLFAPIYVLDYLNETOQLTP
MONTQNLLOMPYGCCEONMVLFAPIYVLDYLNETOQLTP
MONTQNLLOMPYGCCEONMVLFAPIYVLDYLNETOQLTP
MONTQNLLOMPYGCCEONMVLFAPIYVLDYLNETOQLTP

NOV2
gi | 14765710 |
gi | 4557225 |
gi | 224053 |
gi | 6978425 |
gi | 2144118 |

1050 1060 1070 1080
.....|.....|.....|.....|.....|.....|.....|.....|
EIRSRVAGGLEIGYQKGLMYKHSNGSYSAFGERDG--NGN
EIKSKAIGYLNITGYQROLNYKHVDGSYSTEGERYGRNOGN
EIKSKAIGYLNITGYQROLNYKHVDGSYSTEGERYGRNOGN
EIKSKAIGYLNITGYQROLNYKHVDGSYSTEGERYGRNOGN
EIKSKAIGYLNITGYQROLNYKHVDGSYSTEGERYGRNOGN
EIKSKAIGYLNITGYQROLNYKHVDGSYSTEGERYGRNOGN

NOV2
gi | 14765710 |
gi | 4557225 |
gi | 224053 |
gi | 6978425 |
gi | 2144118 |

1090 1100 1110 1120
.....|.....|.....|.....|.....|.....|.....|.....|
TWLTAFVTKCFGQAOAKGIFIDPKNIQDALQWMAGNOLPSG
TWLTAFVLKTEFAQARAYIFIDEAHITOALWLSOROKDNG
TWLTAFVLKTEFAQARAYIFIDEAHITOALWLSOROKDNG
TWLTAFVLKTEFAQARAYIFIDEAHITOALWLSOROKDNG
TWLTAFVLKTEFAQARAYIFIDEAHITOALWLSOROKDNG
TWLTAFVLKTEFAQARAYIFIDEAHITOALWLSOROKDNG

NOV2
gi | 14765710 |
gi | 4557225 |
gi | 224053 |
gi | 6978425 |
gi | 2144118 |

1130 1140 1150 1160
.....|.....|.....|.....|.....|.....|.....|.....|
CYAVGNNLLETAIKGGVDEVSLLAYUTALLENMGKD VDD
CFRSSGSLNNAIKGGVEDEVTLISAYITIALLEPLTVTH
CFRSSGSLNNAIKGGVEDEVTLISAYITIALLEPLTVTH
CFRSSGSLNNAIKGGVEDEVTLISAYITIALLEPLTVTH
CFRSSGSLNNAIKGGVEDEVTLISAYITIALLEPLTVTH
CFRSSGSLNNAIKGGVEDEVTLISAYITIALLEPLTVTH

NOV2
gi | 14765710 |
gi | 4557225 |
gi | 224053 |
gi | 6978425 |
gi | 2144118 |

1170 1180 1190 1200
.....|.....|.....|.....|.....|.....|.....|.....|
PMVSQGLRCLNSATST-----ENLYTOALLAYIESLAG
PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG

NOV2
gi | 14765710 |
gi | 4557225 |
gi | 224053 |
gi | 6978425 |
gi | 2144118 |

1210 1220 1230 1240
.....|.....|.....|.....|.....|.....|.....|.....|
EMDIRNITLKLQDQOATISGESYWSOKPTPSSNASPWSE
NQDKRKEVLKSLNEEAVKQNSVHWERPQKPKAPVGHYE
NQDKRKEVLKSLNEEAVKQNSVHWERPQKPKAPVGHYE
NQDKRKEVLKSLNEEAVKQNSVHWERPQKPKAPVGHYE
NQDKRKEVLKSLNEEAVKQNSVHWERPQKPKAPVGHYE
NQDKRKEVLKSLNEEAVKQNSVHWERPQKPKAPVGHYE

NOV2
gi | 14765710 |
gi | 4557225 |
gi | 224053 |
gi | 6978425 |
gi | 2144118 |

1250 1260 1270 1280
.....|.....|.....|.....|.....|.....|.....|.....|
PAA--VDEVELTAYALLAOLT-KPSELTOGETAKATSIVAWI
PQAPSAEVEMTSYVLLAYLTAOPAPTSSEDLTSATNIVKWI
PQAPSAEVEMTSYVLLAYLTAOPAPTSSEDLTSATNIVKWI
PQAPSAEVEMTSYVLLAYLTAOPAPTSSEDLTSATNIVKWI
PQAPSAEVEMTSYVLLAYLTAOPAPTSSEDLTSATNIVKWI
PQAPSAEVEMTSYVLLAYLTAOPAPTSSEDLTSATNIVKWI

1290 1300 1310 1320
.....|.....|.....|.....|.....|.....|.....|.....|

Applicants: Guo
U.S.S.N.: 09/981,151

NOV2 AKQHNAAGGFSSTQDTVVALQALQKYATTAMPSS-EEINE
gi | 14765710 | TKQONAGGFSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi | 4557225 | TKQONAGGFSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi | 224053 | TKQONAGGFSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi | 6978425 | TKQONAGGFSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi | 2144118 | TKQONAGGFSSTQDTVVALHALSKYGAATFTRTGKAAQV

1330 1340 1350 1360
NOV2 VKSTENFQRTFNHOSVNRLVFOODLPPNPGMYHLEASG
gi | 14765710 | TISSSGTFSSKFOVDNNRLLLOQVSLPEPPGEYSKVTG
gi | 4557225 | TISSSGTFSSKFOVDNNRLLLOQVSLPEPPGEYSKVTG
gi | 224053 | TISSSGTFSSKFOVDNNRLLLOQVSLPEPPGEYSKVTG
gi | 6978425 | TIRSSSGTFSSKFOVDNNRLLLOQVSLPEPPGEYSKVTG
gi | 2144118 | TIKSSSGTFSSKFOVDNNRLLLOQVSLPEPPGEYSKVTG

1370 1380 1390 1400
NOV2 QGCVYVQTVLRYNILPPTNMKTFSLSVIGKARCEQPTSP
gi | 14765710 | EGCVYLQTSCLKYNILPEKEEFPFALGVQTLPTCDEPKAH
gi | 4557225 | EGCVYLQTSCLKYNILPEKEEFPFALGVQTLPTCDEPKAH
gi | 224053 | EGCVYLQTSCLKYNILPEKEEFPFALGVQTLPTCDEPKAH
gi | 6978425 | EGCVYLQTSCLKYNILPEKEEFPFALGVQTLPTCDEPKAH
gi | 2144118 | EGNVYLQTSCLKYNILPEKEEFPFALGVQTLPTCDEPKAH

1410 1420 1430 1440
NOV2 RSLTHTHTSYVGSRSSNMAIVVKMISGFSPHGTNOL
gi | 14765710 | TSFQISLSVSYTGSRSSNMAIVDKMVS GF I PLKPTVKM
gi | 4557225 | TSFQISLSVSYTGSRSSNMAIVDKMVS GF I PLKPTVKM
gi | 224053 | TSFQISLSVSYTGSRSSNMAIVDKMVS GF I PLKPTVKM
gi | 6978425 | TSFQISLSVSYTGSRSSNMAIVDKMVS GF I PLKPTVKM
gi | 2144118 | TSFQISLSVSYTGSRSSNMAIVDKMVS GF I PLKPTVKM

1450 1460 1470 1480
NOV2 LLSQPLVKRVEFGTDTENIYLDLKNQTYTFTISOSVL
gi | 14765710 | LERSNHVSRTEVSSNHVLIYLDKVS NQTLSLFTVQODVP
gi | 4557225 | LERSNHVSRTEVSSNHVLIYLDKVS NQTLSLFTVQODVP
gi | 224053 | LERSNHVSRTEVSSNHVLIYLDKVS NQTLSLFTVQODVP
gi | 6978425 | LERSNHVSRTEVSSNHVLIYLDKVS NQTLSLFTVQODVP
gi | 2144118 | LERSNHVSRTEVSSNHVLIYLDKVS NQTLSLFTVQODVP

1490 1500 1510 1520
NOV2 VRLKPAIVKVYDYETGEFAIAEYNAPCSKDLGNA----
gi | 14765710 | VRLKPAIVKVYDYETGEFAIAEYNAPCSKDLGNA----
gi | 4557225 | VRLKPAIVKVYDYETGEFAIAEYNAPCSKDLGNA----
gi | 224053 | VRLKPAIVKVYDYETGEFAIAEYNAPCSKDLGNA----
gi | 6978425 | VRLKPAIVKVYDYETGEFAIAEYNAPCSKDLGNA----
gi | 2144118 | VRLKPAIVKVYDYETGEFAIAEYNAPCSKDLGNA----

1530 1540
NOV2 ARHPEPPPPFKTEAFIPSLPGSVNN (SEQ ID NO:10)
gi | 14765710 | ----- (SEQ ID NO:35)
gi | 4557225 | ----- (SEQ ID NO:36)
gi | 224053 | ----- (SEQ ID NO:37)
gi | 6978425 | ----- (SEQ ID NO:38)
gi | 2144118 | ----- (SEQ ID NO:39)

Pages 45, please replace Table 2E with the following

Table 2E Domain Analysis of NOV2

gnl|Pfam|pfam00207, A2M, Alpha-2-macroglobulin family. This family includes the C-terminal region of the alpha-2-macroglobulin family. (SEQ ID NO:80)

CD-Length = 751 residues, 98.5% aligned

Score = 563 bits (1451), Expect = 2e-161

Query:	728	EDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITEWKAMSFCTSQSRGFGLSPTVGL	787
		+ + + ++ + ++ + + ++ ++ ++	
Sbjct:	4	DDITIRSYFPESWLWEVEEVDRSPVLTVNITLPDSITTWEILAVSLSNTKGLCVADPVEL	63
Query:	788	TAFKPFFVDLTLPYSVVRGESFRLTATIFNYL-KDCIRVQTDLAKSHEYQLESWADSQTS	846
		+ ++ ++ +	
Sbjct:	64	TVFQDFFLELRPLYSVVRGEQVELRAVLNYLPSQDIKV-----VVQLEVEPLCQAG	115
Query:	847	SCLCADDAKTHHWNITAVKLGHINFITISTKILDSNEPCGGQKGFVPQKGRSDTLIKPVLV	906
		++ ++ + + ++ +	
Sbjct:	116	FCSLATQTRSSQSVRPKSLSSVSFPVVVPLASGLSLVEVVASVPEFFVKDAVVKTLKV	175
Query:	907	KPEGVLVEKTHSSLLCP---KGGKVASESVSLELPVDIVPD-STKAYVTVLGDIMGTAQ	962
		+ + + + ++ + +	
Sbjct:	176	EPEGARKEETVSSLLLPEHLGGGLEVSEVPALKLPDDVPDTEAEAVISVQGDPVAQAIQ	235
Query:	963	N-----LDGLVQMPSGCGEQNMVLFAPIIYVLOYLEKAGLLTE---EIRSRAVGFLSIG	1013
		+ +++ + + ++ + + + + +	
Sbjct:	236	NTLSGEGLNNLLRLPSGCGEQNMIYMAPTVYVLHYLDETQWEKPGTKKKQKAIDLKNG	295
Query:	1014	YQKELMYKHSNGSYSAFGERDGNNGNTWLTAFTVKCFGQAQKFIFIDPKNIQDALKW-MAG	1072
		++ + ++ + + + ++ ++ + +	
Sbjct:	296	YQRQLNYRKADGSYAAFLHRA--SSTWLTAFLVKVFSQARNYVFIDEEHICGAVKWLILN	353
Query:	1073	NQLPSGCYANVGNLLHTAMKGGVDD---EVSLTAYVTAALLEMGKDVDPMVVSQGLRCL	1128
		+ + ++ ++ ++ + +	
Sbjct:	354	QQKDDGVFRESGPVIHNEMKGGVGDDAEVEVTLTAFITIALLEAKLVCISPVVANALSIL	413
Query:	1129	KNSATSTTN-----LYTQALLAYIFSLAGEMDIRNILLKQLDQQAIISGESIYWS--QK	1180
		+ + + ++ + +	
Sbjct:	414	KASDYLLENYANGQRYVTLALTAYALALAGVLHKLKEILKSLKEELYKALVKGHWERPQK	473
Query:	1181	PTPSSNASPWSEPAAVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNAVGGS	1240
		+ + + + ++ + +	
Sbjct:	474	PKDAPGHPYSPQPQAAAVEMTSYALLALLT--LLPFPKVEMAPKVVKWLTEQQYYGGGFG	531
Query:	1241	STQDTVVALQALAKYATTAYMPSE-EINLVVKSTEN-FQRTFNIQSVNRLVFQQDTLP-N	1297
		+ + ++ ++ + + + +	
Sbjct:	532	STQDTVMALQALSKYGIATPTHKEKNLSVTIQSPSGSFKSHFQILNNNAFLLRPVELPLN	591
Query:	1298	VPGMYTLEASGQGCYVQTVLRYNLPPTNMKTFSLSVEIGKARCEQPTSPR-SLTLTIH	1356
		+ + + + + + + + +	
Sbjct:	592	EGFTVTAKVTGQGTLLVTTRYRYKVLDDKNTFCFDLKIETVPDTCVEPKGAKNSDYLIC	651
Query:	1357	TSYVGSRSSSNMAIVEVKMLSGFSPMEGT--NQLLLQQLPVKKVEFGTDTLNIYLDLILK	1414
		++ + ++ + + + ++	
Sbjct:	652	TRYAGSRSDSGMAIADISMLTGFIPLKPDLLKLENGVDRYVSKYEIDGNHVLLYLDKVSH	711
Query:	1415	-NTQTYTFTISQSVLVTNLKPATIKVYDYLLP 1445 (of SEQ ID NO:10)	
		+ + ++	

Applicants: Guo
U.S.S.N.: 09/981,151

Sbjct: 712 SETECVGFKIHQDFEVGLLQPASVKVYDYEP 743 (SEQ ID NO:80)

Pages 46, please replace Table 2F with the following:

Table 2F Domain Analysis of NOV2

gnl|Pfam|pfam01835, A2M_N, Alpha-2-macroglobulin family N-terminal region. This family includes the N-terminal region of the alpha-2-macroglobulin family. (SEQ ID NO:81)
CD-Length = 620 residues, 98.4% aligned
Score = 236 bits (603), Expect = 5e-63

Query:	5	LLLGMLALSPAIAEEL--PNYLVTLPARLNFPSVQKVCLDLSPGYSDVKFTVTLETKDKT	62
		+ + + + + + + + +	
Sbjct:	2	LLWLLLLLLLLFFDSSLQKPRYMVIVPSILRTETPEKVCVQLHDLNETVTVTVSLHSFPGK	61
Query:	63	QKLLEYSGLK---KRHLHCISFLVPPPA---GGTEEVATIRVSGVGNNISFEEKKKVLIQ	116
		+ + + + + + + +	
Sbjct:	62	RNLSSLFTVLLSSKDLFHCVSFTVPQPGLFKSSKGEESFVVVQVKGPTHTFKEKVTVLVS	121
Query:	117	RQNGTTFVQTDKPLYTPGQQVYFRIVTMDSNFVPVNDKYSMVELQDPNSNRIAQWLEVVP	176
		+ + + + + + + + + +	
Sbjct:	122	SRRGLVFIQTDKPIYTPGQTVRYRVFSVDENLRPLNELI-LVYIEDPEGNRVDQWEVNKL	180
Query:	177	EQGIVDLSFQLAPEAMLGTYTVAV---AEGKTFGT--FSVEEYVLSPFLLLLSSVLPKFK	231
		+ + + + + + + + +	
Sbjct:	181	EGGIFQLSFPIPSEPIQGTWKIVARYESGPESNYTHYFEVKEY-----VLPSFEVS	231
Query:	232	VEVVEPKELSTVQESFLVKICCRYTYGKPMLGAVQVSVCQKANTYWYREVEREQLPDKCR	291
		+ + + + + + +	
Sbjct:	232	ITPPKPFIIYDNFKEFEVTICARYTYGKPVPGVAYVRFGVK-----DEDGKKELLAGLE	285
Query:	292	NLSGQTDKTG--CFSAPVDMATFDLIGYAY-SHQINIVATVVEEGTGVEANA-TQNIYIS	347
		+ + + + +	
Sbjct:	286	ERAKLLDGNGEICLSQEVLLKELQLKNEDLEGKSLYVAVAVIESEGDMEEAELGGIKIV	345
Query:	348	PQMGSMTFEDTSNFIHPNFPFSGKMLLKFPQGGVLPCKNHLVFLVIYGTNGTFNQTLVTD	407
		+ + + + + + + + +	
Sbjct:	346	RSPYKLFVKTPSHFKPGIPFFLKVLVVDPDGS--PAPNVPVK--VSAQDASYYSNGTTD	401
Query:	408	NNGLAPFTLETSGWNGTDVSLEGKFQMEDLVYNPEQVPRYYQNAYLHLRPFYSTTRSFLG	467
		+ + + + + + + + + + + +	
Sbjct:	402	EDGLAQFSINTS--GISSLSITVRTNHKELPEEVQAHAEAQATAYSTVSL--SKSYIHLS	457
Query:	468	IHLNGLPLKCGQPQEVLDVYYIDPADASPDQEISFSYYLIGKGSVMQKHLNSKKKGL	527
		+ + + + + + + + + + + + +	
Sbjct:	458	IER---TLPCGPGVGEQANFILRGKSLGELKILHFYYLIMSKGKIVKTGRE----PREPG	510
Query:	528	KASFSLSLTFTSRLAPDPSLVIYAIFPSGGVVADKIQFSVEMCFDN-----QQL	576
		+ + + +	
Sbjct:	511	QGLFSLSIPVTPDLAPSFRLVAYYILPQGEVVADSVWIDVEDCCANKLDLSFSPSKDYRL	570
Query:	577	PGALEVELQLQAAPGSLCALRAVDESLLLLRPDRELSNRSVY	617 (of SEQ ID NO:10)
		+ + + + + + + +	
Sbjct:	571	PAQQVKLRVEADPQSLVALRAVDQAVYLLKPKAKLSMSKVY	611 (SEQ ID NO:81)

Applicants: Guo
U.S.S.N.: 09/981,151

At page 52 please replace Table 3E with the following:

Table 3E. BLAST results for NOV3					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
<u>gi 12858115 dbj BAB31203.1 </u> (AK018423) BAB31203	putative [Mus musculus]	373	187/310 (60%)	226/310 (72%)	6e-87
<u>gi 3024224 sp Q28727 NTCI-RABIT</u> NP 058918	ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM- DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAURO CHOLATE COTRANSPORTIN G POLYPEPTIDE, ILEAL)	347	116/279 (41%)	173/279 (61%)	1e-52
<u>gi 8394281 ref NP-058918.1 </u> NP 035518	solute carrier family 10, member 2 [Rattus norvegicus]	348	130/344 (37%)	195/344 (55%)	2e-52
<u>gi 6755530 ref NP-035518.1 </u> NP 35518	solute carrier family 10, member 2 [Mus musculus]	348	125/313 (39%)	191/313 (60%)	4e-52
<u>gi 6755530 ref NP-035518.1 </u> NP 35518	solute carrier family 10, member 2 [Mus musculus]	348	125/313 (39%)	191/313 (60%)	4e-52

Applicants: Guo
U.S.S.N.: 09/981,151

<u>gi 2842631 sp Q60414 NTCI-CRIGR</u> <u>Q60414</u>	ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM- DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAURO CHOLATE COTRANSPORTIN G POLYPEPTIDE, ILEAL)	348	121/306 (39%)	185/306 (59%)	4e-52
---	--	-----	------------------	------------------	-------

At page 53 please replace Table 3F with the following:

Table 3F. ClustalW Analysis of NOV3

- 1) NOV3 (SEQ ID NO:12)
- 3) gi|12858115|dbj|BAB31203.1| gi|12858115| BAB31203 (AK018423) putative [Mus musculus] (SEQ ID NO:40)
- 4) gi|3024224|sp|Q28727|NTCI-RABIT gi|3024224| NP058918 ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL) (SEQ ID NO:41)
- 5) gi|8394281|ref|NP_058918.1| gi|8394281| NP035518 solute carrier family 10, member 2 [Rattus norvegicus] (SEQ ID NO:42)
- 6) gi|6755530|ref|NP_035518.1| gi|6755530| NP035518 solute carrier family 10, member 2 [Mus musculus] (SEQ ID NO:43)
- 7) gi|6755530|ref|NP_035518.1| gi|6755530| NP035518 solute carrier family 10, member 2 [Mus musculus] (SEQ ID NO:44)
- 8) gi|2842631|sp|Q60414|NTCI-CRIGR gi|2842631| Q60414 ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL) (SEQ ID NO:45)

	10	20	30	40
NOV3			
gi 12858115	MRA N CS-S S SACPANSS E E E PPVGL E V E GN L E V F I V S T			
gi 3024224	MSTDCA-GNSTCPVNST E EDPPVGM E GHAN L K L L F I V LSA			
gi 8394281	MSNL I V G CLANATVCEGASCVAPESN F NA I LSV V STVLT			
gi 6755530	MONSSV-CSPNAT F CEG D SC I V T ESN F NA I LS T VMSTVLT			
gi 2842631	MONSSV-CPPNATVCEG D SC V VPESN F NA I LS T VMSTVLT			
	MONSSI-CNP N AT I CEG D SC I APESN F NA I LS V VMSTVLT			
	50	60	70	80
NOV3			
gi 12858115	TMGL L MF S FGCSVE R RKLWSH I RRPWG I AVGL L CQ F GM			
	VMGLV M FSFGCSVES O KLWLH I RRPWG I AVGL L SQ F GM			

Applicants: Guo
U.S.S.N.: 09/981,151

gi | 3024224 | ILLALVMFSMGCNVEKFLGHIRRPWGIIVGFLCQFGIM
gi | 8394281 | ILLALVMFSMGCNVEKFLGHIRRPWGIIVGFLCQFGIM
gi | 6755530 | ILLALVMFSMGCNVEKFLGHIRRPWGIIVGFLCQFGIM
gi | 2842631 | ILLALVMFSMGCNVEKFLGHIRRPWGIIVGFLCQFGIM

NOV3
gi | 12858115 | PFTAMT LAISFSIRKPVOAIAVLIMGCCRG---APSLTSP
gi | 3024224 | PLTAMT LAIGFGKPKFOAIAVLIMGSCPGGTISNVLTFWV
gi | 8394281 | PLTGFVLVAFGIIPVOAVVVLIMGCCPGGTASNILAYWV
gi | 6755530 | PLTGFVLVAFGIIPVOAVVVLIMGCCPGGTASNILAYWV
gi | 2842631 | PLTGFVLVAFGIIPVOAVVVLIMGCCPGGTASNILAYWV

NOV3
gi | 12858115 | SGLMTHWISG-----ALGMMPLCLVLYTWSWSLQONIT
gi | 3024224 | DGDMDLSISMTTCSTLLALGMMPLCLVLYTKMWVDSGTIV
gi | 8394281 | DGDMDLSVSMITTCSTLLALGMMPLCLVLYTKMWVDSGTIV
gi | 6755530 | DGDMDLSVSMITTCSTLLALGMMPLCLVLYTKMWVDSGTIV
gi | 2842631 | DGDMDLSVSMITTCSTLLALGMMPLCLVLYTKMWVDSGTIV

NOV3
gi | 12858115 | IPYONIGLSIGILVCLTIPVAFGVVNVWPQKSKILK
gi | 3024224 | IPYQ----SIGILVSLVVPVASGVVNVWPQKATVILK
gi | 8394281 | IPYD----NIGTSLVALVIPVSI GMVNHKWPQKAKIILK
gi | 6755530 | IPYD----SIGISLVALVIPVSI GMVNHKWPQKAKIILK
gi | 2842631 | IPYD----SIGTSLVALVIPVSI GMVNHKWPQKAKIILK

NOV3
gi | 12858115 | --AVVGGVLLVAVAGVVLAKGSWNSDITLTISFIFPI
gi | 3024224 | VGAILGGMILLVAVTGMVLAAG-WNTDVTLLVISCFPI
gi | 8394281 | VGSIAGAVLIVLIAVVGGLYQSAWIIEPKLWIIGTIFPI
gi | 6755530 | VGSITGVLLIVLIAVVGGLYQSAWIIEPKLWIIGTIFPI
gi | 2842631 | VGSIAGAVLIVLIAVVGGLYQSAWIIEPKLWIIGTIFPI

NOV3
gi | 12858115 | IGEVTGFLALFTHQSWQ--RTIPFLGLAFKTPCDTILA
gi | 3024224 | VGEVTGFLALFTHQSWQRCRTISITETGAONIQLCIAMTQ
gi | 8394281 | AGYSLGFFLARLAGQPWYRCRTVALETGMONTQLCSTIVQ
gi | 6755530 | AGYSLGFFLARLAGQPWYRCRTVALETGMONTQLCSTIVQ
gi | 2842631 | AGYGLGFFLARLAGQPWYRCRTVALETGMONTQLCSTIVQ

NOV3
gi | 12858115 | MSCEPCSRLLIYAFIPLLYGTFQVMDGFLIIVEE-----
gi | 3024224 | LSFSAEYLVQLNFA-LAYGTFQVMDHGLIIVAAAYQAYKRR
gi | 8394281 | LSFSPEDLTIVFTFP-LIYSIFQVAFAAFLGIYVAYKRC
gi | 6755530 | LSFSPEDLNLVFTFP-LIYVTFQVFAAVILGIYVTYKRC
gi | 2842631 | LSFSPEDLNLVFTFP-LIYSIFQVAFAAFLGAYVAYKRC

NOV3
gi | 12858115 | -----RTEDTDC-----EGSP--LPEVFT-----EVTIIP
gi | 3024224 | QKSKCRRQHPDCPDVCYKOPRETSFLLDKGDEAAVNLGP
gi | 2842631 | EG-KNDAEFPDIKDT--KTEP--ESSFHO-----MNGG

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi|8394281|      EG-KNDAEFLKTDN--DMDP--MPSFQ-----TNKG
gi|6755530|      YG-KNDAEFLKTDN--EMDS--RPSFD-----TNKG
gi|2842631|      EG-KNNTeloKTDN--EMEP--RSSFQ-----TNKG
```

```

              370      380
      ....|....|....|....|
NOV3      KQPRI----- (SEQ ID NO:12)
gi|12858115| VQPEQHRAAELTSHIPSC (SEQ ID NO:40)
gi|3024224|  FQPE----- (SEQ ID NO:41)
gi|8394281|  FQPD EK----- (SEQ ID NO:42)
gi|6755530|  FQPD EK----- (SEQ ID NO:43)
gi|2842631|  FQPD EK----- (SEQ ID NO:45)
```

Page 55, please replace Table 3G with the following

Table 3G Domain Analysis of NOV3

gnl|Pfam|pfam01758, SBF, Sodium Bile acid symporter family. This family consists of Na+/bile acid co-transporters. These transmembrane proteins function in the liver in the uptake of bile acids from portal blood plasma a process mediated by the co-transport of Na+. Also in the family is ARC3 from S. cerevisiae this is a putative transmembrane protein involved in resistance to arsenic compounds. (SEQ ID NO:82)

CD-Length = 186 residues, 80.1% aligned

Score = 75.9 bits (185), Expect = 3e-15

```

Query:  39  TIMMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFGLMPFTAYLLAIS-FSLKPVQA  97
          + + | + | | + | | | + | | | + + | | + + | | | |
Sbjct:   1  ALGLFLMMFSMGLKVRFEDLKEALRRPKALILGLLLQWIIMPLLMFILAWLLLRLPPELA  60

Query:  98  IAVLIMCCRG---APSLTFSPSGLMEIWIS-----GALGMMPLCIYLYTWSWSLQQN  147
          + + + + | | + | + | + + + + | + | | + |
Sbjct:  61  TGLILVGCAPGGAMSNVWTYLAKGDVELSVVMVALSTLLAPLVTPLLSFLLAGLL-----  115

Query: 148  LTIPYQNIGLSLGITLVCLTIPVAFGVVYVNYRWP  181  (of SEQ ID NO:12)
          + + + + | | + | | + | + | |
Sbjct: 116  VHDAVSPWSLIKSVLVYVVIPLIAGMLTRYFLP  149  (SEQ ID NO 82)
```

At page 61, please replace Table 4C with the following:

Table 4C. BLAST results for NOV4					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 4505773 ref NP_002625.1 NP 002625	prohibitin [Homo sapiens]	272	236/270 (87%)	251/270 (92%)	e-123
gi 92643 pir A39682	prohibitin - rat	272	235/270 (87%)	251/270 (92%)	e-123

Applicants: Guo
U.S.S.N.: 09/981,151

<u>gi 7298546 gb AAF53765.1 </u> (<u>AE003661</u>) <u>AAF53765</u>	1(2)37Cc gene product [Drosophila melanogaster]	276	178/270 (65%)	220/270 (80%)	8e-96
<u>gi 2055454 gb AAB53231.1 </u> (<u>U97204</u>) <u>AAB53231</u>	prohibitin-like molecule TC-PRO-1 [Toxocara canis]	274	153/264 (57%)	209/264 (78%)	9e-80
<u>gi 13491275 gb AAK27865.1 </u> (<u>AC087079</u>) <u>AAK27865</u>	Hypothetical protein Y37E3.9 [Caenorhabditis elegans]	275	154/270 (57%)	210/270 (77%)	6e-79

At page 61 please replace Table 4D with the following:

Table 4D ClustalW Analysis of NOV4

- NOV4 (SEQ ID NO:14)
- gi|4505773|ref|NP_002625.1| NP 002625 gi|4505773| prohibitin [Homo sapiens] (SEQ ID NO:46)
- gi|92643|pir|A39682 A39682 gi|6679299| prohibitin - rat (SEQ ID NO:47)
- gi|7298546|gb|AAF53765.1| AAF53765 (AE003661) gi|7298546| 1(2)37Cc gene product [Drosophila melanogaster] (SEQ ID NO:48)
- gi|2055454|gb|AAB53231.1| AAB53231 (U97204) gi|2055454| prohibitin-like molecule TC-PRO-1 [Toxocara canis] (SEQ ID NO:49)
- gi|13491275|gb|AAK27865.1| AAK27865 (AC087079) gi|13491275| Hypothetical protein Y37E3.9 [Caenorhabditis elegans] (SEQ ID NO:50)

	10	20	30	40
NOV4	MAAKVFESIGKFGGLALVAGGVVNSALYSVDAGHRAV		
gi 4505773	MAAKVFESIGKFGGLALVAGGVVNSALYNVDAGHRAV		
gi 6679299	MAAKVFESIGKFGGLALVAGGVVNSALYNVDAGHRAV		
gi 7298546	MAAOFENRIGOMGLGVAVLGGVVNSALYNVEGGHRAV		
gi 2055454	MAGAOKILGRVGGIGVALAVTGGVVNSALYNVDGGRRAV		
gi 13491275	MAASAOKILGRVGTGVGLSTAGGTAQALYNVDGGRRAV		
	50	60	70	80
NOV4	IFDRFRGVQDIVVGKGTGTHCLIPWVOKSIIFDCRSQPRNVP			
gi 4505773	IFDRFRGVQDIVVGEGTGHFLIPWVOKPIIFDCRSRPRNVP			
gi 6679299	IFDRFRGVQDIVVGEGTGHFLIPWVOKPIIFDCRSRPRNVP			
gi 7298546	IFDRFTGLKENNVVGEGTGHFLIPWVORPIIFDIRSQPRNVP			
gi 2055454	IFDRFTGVKPDVVVGEGTGHFLIPWVORPIIFDIRSTPRATS			
gi 13491275	IFDRFSGVKNENVVGEGTGHFLIPWVOKPIIFDIRSTPRAVT			
	90	100	110	120
NOV4	VITGSKDLQNVNITLRILRRPVASQLPHIETSSGEDYDER			
gi 4505773	VITGSKDLQNVNITLRILRRPVASQLPRIETSSIGEDYDER			
gi 6679299	VITGSKDLQNVNITLRILRRPVASQLPRIYTSIGEDYDER			
gi 7298546	VITGSKDLQNVNITLRILRRPDPDLPKIYTIIGODYDER			
gi 2055454	TITGSKDLQNVNITLRILRRPEPSKLPNIYLNIGODYAER			
gi 13491275	TITGSKDLQNVNITLRILRRPSPDRLPNIYLNIGLDYAER			
	130	140	150	160
NOV4	VLPSITNEVLKAVVAQFDAGELITOREQVSROVSDDLTER			
gi 4505773	VLPSITNEVLKAVVAQFDAGELITORELVSROVSDDLTER			
gi 6679299	VLPSITNEVLKAVVAQFDAGELITORELVSROVSDDLTER			
gi 7298546	VLPSIAPEVLKAVVAQFDAGELITOREMVSQVSOELTVR			
gi 2055454	VLPSITNEVLKAVVAQFDAGELITORESVSERVSVELSER			
gi 13491275	VLPSITNEVLKAVVAQFDAGELITOREVVSQKASVALRER			

Applicants: Guo
U.S.S.N.: 09/981,151

	170	180	190	200	
NOV4	
gi 4505773	AATFGLILDDVSLTTLTFGKEFTEAVEAKQIAQQEAEERAR				
gi 6679299	AATFGLILDDVSLTTLTFGKEFTEAVEAKQIAQQEAEERAR				
gi 7298546	AATFGLILDDVSLTTLTFGKEFTEAVEAKQIAQQEAEERAR				
gi 2055454	AKQFGFLLDDVSLTTLTFGREFTLAVEMKQVAQQEAEERAR				
gi 13491275	AAQFGLLLDDVSLTTLTFGREFTLAVEMKQVAQQEAEERAR				
	210	220	230	240	
NOV4	
gi 4505773	FVVEKAEQOKKAAIISAEGDSKVAELITNSLATAGDALIE				
gi 6679299	FVVEKAEQOKKAAIISAEGDSKVAELITNSLATAGDGLIE				
gi 7298546	FVVEKAEQOKKAAIISAEGDSKVAELITNSLATAGDGLIE				
gi 2055454	FVVEKAEQOKKAAIISAEGDAEAAGLIAKSFGEAGDGLVE				
gi 13491275	FVVEKAEQOKKAAIISAEGDAEAAGLIAKSFGEAGDGLVE				
	250	260	270		
NOV4		
gi 4505773	LRKIEAEDITVQLRSRNTIYLRAGQSMPLQLRW----			(SEQ ID NO:14)	
gi 6679299	LRKIEAEDITVQLRSRNTIYLRAGQSVLLQLPQ----			(SEQ ID NO:46)	
gi 7298546	LRKIEAEDITVQLRSRNTIYLRAGQSVLLQLPQ----			(SEQ ID NO:47)	
gi 2055454	LRKIEAEDITVQLRSRNVAYLPSGOSTHNLPLSTIAQ			(SEQ ID NO:48)	
gi 13491275	LRKIEAEDITVQLRSRNVAYLPSGOSTHNLPLSTIAQ			(SEQ ID NO:49)	
	LRKIEAEDITVQLRSRNVAYLPSGOSTHNLPLSTIAQ			(SEQ ID NO:50)	

At page 62 please replace Table 4E with the following:

Table 4E. Domain Analysis of NOV4	
gi Pfam pfam01145, Band_7, SPFH domain / Band 7 family. This family also includes proteins with high blast scores to known Band 7 protein: HflC from E. coli HflK from E. coli, and Prohibitin family members (SEQ ID NO:83)	
CD-Length = 191 residues, 91.6% aligned	
Score = 157 bits (397), Expect = 7e-40	

Query:	28	YSVDAGHRAVVFDRFRGVQDIVVGKGTCLIPWLQKSIIFDCRSQPRNVPVITGSKDLQN	87
		+ + + + + + +	
Sbjct:	17	KIVKEYERGVI FRLGRYVRQ-VVG PGLHFIIPFIDTVKKVDLRTVVYDVPSQEII TKDNV	75
Query:	88	VNLT LR IIFRPVASQLPHIFTSSGEDHDERVPPSITNKILKSVVARFEAGELITQREQIS	147
		+ + + + + + + + + + + + + + + + +	
Sbjct:	76	VVIVDAVVYYRVVDPLKAVYEVED---AERALPQLAQTTLRNVIGQFTLDEILTERERIN	132
Query:	148	RQVSDDLTEPAATFGLILDDVSLTTLTFGKEFTEAVEAKQIAQQEAEERARFVVEKAEQOK	207
		+ + + + + + + + + + + + + + + + +	
Sbjct:	133	SQLREILDEATDPWGIKVERVEIKDIRLP EEVQRAMAAQMEAEAREA-RAKILEAEGEQEA	191
Query: (aa 28-207 of SEQ ID NO:14)			
Sbjct: (SEQ ID NO:83)			

Applicants: Guo
U.S.S.N.: 09/981,151

At page 63, please replace Table 4F with the following:

Table 4F. Domain Analysis of NOV4	
gnl Smart smart00244	PHB, prohibitin homologues; prohibitin homologues (SEQ ID NO:84)
CD-Length = 160 residues, 98.8% aligned	
Score = 97.4 bits (241), Expect = 9e-22	

Query: 28 YSV DAGHRAVVFDRFRGVQDIVVGKGTCLIPWLQKSIIFDCRSQPRNVPVITG-SKDLQ 86
+ | | | + | | | + | | | + | | + | | + | |
Sbjct: 3 FYVIGEGERGVERLGRVLK-VLGPGLHFVIPFIDDVKRVDLRAQTDDVPPQEVITKDNV 61

Query: 87 NVNLTLRRIIFRPVASQLPHIFTSSGEDHDERVPPSITNKILKSVVARFEAGELIT-QREQ 145
|++ + + | | | ++ | | | + | + | + | + | + | + |
Sbjct: 62 TVSVDAVVYR-VLDPLKAVYGV--LDADYRALRQLAQTTLRSVIGKRTLDELLTDEREK 118

Query: 146 ISRQVSDDLTEPAATFGLILDDVSLTYLTFGKEFIEAVEAKQ 187 (of SEQ ID NO:14)
| | + ++ | | | + | + ++ | | + + + | | + | + |
Sbjct: 119 ISENIREELNEAAEPWGIEVEDVEIKDIRLP EEIKEAMEAQQ 160 (SEQ ID NO:84)

At page 67 please replace Table 5C with the following:

Table 5C. BLAST results for NOV5					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 15294659 ref XP_054070.1 XP 05407	macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens]	711	561/720 (77%)	577/720 (79%)	0.0
gi 10337615 ref NP_066278.1 NP 066278	macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens]	711	560/720 (77%)	576/720 (79%)	0.0
gi 123114 sp P26927 HGFL_HUMAN-P26927	HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (MACROPHAGE STIMULATORY PROTEIN) (MSP) (MACROPHAGE STIMULATING PROTEIN)	711	560/720 (77%)	576/720 (79%)	0.0
gi 15299258 ref XP_017811.2 XP 017811	hypothetical protein XP_017811 [Homo sapiens]	529	440/532 (82%)	456/532 (85%)	0.0
gi 90615 pir A40332 A40332	macrophage-stimulating protein 1 precursor - mouse	716	449/725 (61%)	507/725 (69%)	0.0

Applicants: Guo
U.S.S.N.: 09/981,151

At page 68 please replace Table 5D with the following:

Table 5D Clustal W Sequence Alignment

- 1) NOV5 (SEQ ID NO:16)
- 2) ~~gi|15294659|ref|XP_054070.1|~~ gi|15294659| XP 05407 macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens] (SEQ ID NO:51)
- 3) ~~gi|10337615|ref|NP_066278.1|~~ gi|10337615| NP 066278 macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens] (SEQ ID NO:52)
- 4) ~~gi|123114|sp|P26927|HGF-L HUMAN~~ gi|123114| P26927 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (MACROPHAGE STIMULATORY PROTEIN) (MSP) (MACROPHAGE STIMULATING PROTEIN) (SEQ ID NO:53)
- 5) ~~gi|15299258|ref|XP_017811.2|~~ gi|15299258| XP 017811 hypothetical protein XP_017811 [Homo sapiens] (SEQ ID NO:54)
- 6) ~~gi|90615|pir|A40332~~ gi|90615| A40332 macrophage-stimulating protein 1 precursor - mouse (SEQ ID NO:55)

	10	20	30	40
NOV5
gi 15294659	MGWLP	LLLLLT	QCLGV	PGQ
gi 10337615	MGWLP	LLLLLT	QCLGV	PGQ
gi 123114	MGWLP	LLLLLT	QCLGV	PGQ
gi 15299258	MGWLP	LLLLLT	QCLGV	PGQ
gi 90615	MGWLP	LLLLLT	QCLGV	PGQ

	50	60	70	80
NOV5
gi 15294659	VVPGP	WQEDV	ADAEE	CAGRC
gi 10337615	VVPGP	WQEDV	ADAEE	CAGRC
gi 123114	VVPGP	WQEDV	ADAEE	CAGRC
gi 15299258	VVPGP	WQEDV	ADAEE	CAGRC
gi 90615	VVPGP	WQEDV	ADAEE	CAGRC

	90	100	110	120
NOV5
gi 15294659	LPWTQ	HSPH	TRLR	RSGR
gi 10337615	LPWTQ	HSPH	TRLR	RSGR
gi 123114	LPWTQ	HSPH	TRLR	RSGR
gi 15299258	LPWTQ	HSPH	TRLR	RSGR
gi 90615	LPWTQ	HSPH	TRLR	RSGR

	130	140	150	160
NOV5
gi 15294659	TMATT	VGGP	LCQAW	SHKFP
gi 10337615	TMATT	VGGP	LCQAW	SHKFP
gi 123114	TMATT	VGGP	LCQAW	SHKFP
gi 15299258	TMATT	VGGP	LCQAW	SHKFP
gi 90615	TMATT	VGGP	LCQAW	SHKFP

	170	180	190	200
NOV5
gi 15294659	DGDPG	GPWC	YTTP	DAVRF
gi 10337615	DGDPG	GPWC	YTTP	DAVRF
gi 123114	DGDPG	GPWC	YTTP	DAVRF
gi 15299258	DGDPG	GPWC	YTTP	DAVRF
gi 90615	DGDPG	GPWC	YTTP	DAVRF

	210	220	230	240
--	-----	-----	-----	-----

Applicants: Guo
U.S.S.N.: 09/981,151

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

.....|.....|.....|.....|.....|.....|.....|.....|
GAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYC
GAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYC
GAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYC
GAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYC
GAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYC
GEVDVTESGRECQRWDLQHPHSHPFEPGKFLDQGLDDNYC

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

250 260 270 280
.....|.....|.....|.....|.....|.....|.....|.....|
RNPDGSERPWCYTTPDIEREFCDLPRCG-----SE
RNPDGSERPWCYTTPDIEREFCDLPRCG-----SE
RNPDGSERPWCYTTPDIEREFCDLPRCG-----SE
RNPDGSERPWCYTTPDIEREFCDLPRCG-----SE
RNPDGSERPWCYTTPDIEREFCDLPRCG-----SE
RNPDGSERPWCYTTPDIEREFCDLPSCGPNLPPTVKGSK

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

290 300 310 320
.....|.....|.....|.....|.....|.....|.....|.....|
AOPROEATTVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
AOPROEATTVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
AOPROEATTVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
AOPROEATTVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
AOPROEATTVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
SQRNRKGAENCFRGKGEGYRGTTANTTTAGVPCORWDAQS

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

330 340 350 360
.....|.....|.....|.....|.....|.....|.....|.....|
PHQHRETPEKYACKDLRENFCRNPDGSEAPWCFTLRPGMR
PHQHRETPEKYACKDLRENFCRNPDGSEAPWCFTLRPGMR
PHQHRETPEKYACKDLRENFCRNPDGSEAPWCFTLRPGMR
PHQHRETPEKYACKDLRENFCRNPDGSEAPWCFTLRPGMR
PHQHRETPEKYACKDLRENFCRNPDGSEAPWCFTLRPGMR
PHQHRETPEKYACKDLRENFCRNPDGSEAPWCFTLRPGMR

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

370 380 390 400
.....|.....|.....|.....|.....|.....|.....|.....|
AAFCYQIRRCTDDVRPQATATTAQGSSTAARSAPARVSSA
AAFCYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQC
AAFCYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQC
AAFCYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQC
VGFYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQC
MAFCEQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQC

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

410 420 430 440
.....|.....|.....|.....|.....|.....|.....|.....|
SAGPLRRRTSRSSRLPPNRMHNWRRTSAGTOMGIAMGPGA
QRWSAETPHKPOFTTSEPQAOLEENFCRNPDGDSHGP--
QRWSAETPHKPOFTTSEPQAOLEENFCRNPDGDSHGP--
QRWSAETPHKPOFTTSEPQAOLEENFCRNPDGDSHGP--
QRWSAETPHKPOFTTSEPQAOLEENFCRNPDGDSHGP--
QRWSAETPHKPOFTTSEPQAOLEENFCRNPDGDSHGP--

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

450 460 470 480
.....|.....|.....|.....|.....|.....|.....|.....|
TRITOGPHSTTVPCDAALMTSRHQS--WTPQTCSLRSVA
WCYTMDPRIPFDYCALRRCADDPSPSILDPPDQVFEKCG
WCYTMDPRIPFDYCALRRCADDPSPSILDPPDQVFEKCG
WCYTMDPRIPFDYCALRRCADDPSPSILDPPDQVFEKCG
TRITOGPHSTTVPCDAALMTSRHQS--WTPQTCSLRSVA
WCYTMDPRIPFDYCALRRCADDPSPSILDPPDQVFEKCG

490 500 510 520
.....|.....|.....|.....|.....|.....|.....|.....|

Applicants: Guo
U.S.S.N.: 09/981,151

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

RGWIGWISGVPSCAWEGAIRATHPGQSA CGIG-----
KRVDRLDQRRSKLRVVGHPGNSPWTVSLRNRQGOHFCGG
KRVDRLDQRRSKLRVVGHPGNSPWTVSLRNRQGOHFCGG
KRVDRLDQRRSKLRVVGHPGNSPWTVSLRNRQGOHFCGG
RGWIGWISVVPSCAWEGAIRATHPGQSA CGIGQGOHFCGG
K-----RVDKSNKLRVVGHPGNSPWTVSLRNRQGOHFCGG

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

530 540 550 560
.....|.....|.....|.....|.....|.....
-----MPLTG YEVWLGLTFONPOHGE
SLVKEQWILTAROCFSSCHMPLTG YEVWLGLTFONPOHGE
SLVKEQWILTAROCFSSCHMPLTG YEVWLGLTFONPOHGE
SLVKEQWILTAROCFSSCHMPLTG YEVWLGLTFONPOHGE
SLVKEQWILTAROCFSSCHMPLTG YEVWLGLTFONPOHGE
SLVKEQWILTAROCFSSCHMPLTG YEVWLGLTFONPOHGE
SLVKEQWILTAROCFSSCHMPLTG YEVWLGLTFONPOHGE

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

570 580 590 600
.....|.....|.....|.....|.....|.....
PSLQRPVAKMVCGPSGSQVLVLLKLEKRSVTLNORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEKRSVTLNORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEKRSVTLNORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEKRSVTLNORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEKRSVTLNORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEKRSVTLNORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEKRSVTLNORVALICL

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

610 620 630 640
.....|.....|.....|.....|.....|.....
PPEWYVPPGKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVPPGKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVPPGKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVPPGKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVPPGKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVPPGKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVPPGKCEIAGWGETKGTGNDTVLNVALLNVISN

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

650 660 670 680
.....|.....|.....|.....|.....|.....
QECNIKHRRG-----RGDYGGPLACFT
QECNIKHRRGRVRESEMCTGLAPVGACEGDYGGPLACFT
QECNIKHRRGRVRESEMCTGLAPVGACEGDYGGPLACFT
QECNIKHRRGRVRESEMCTGLAPVGACEGDYGGPLACFT
QECNIKHRRGRVRESEMCTGLAPVGACEGDYGGPLACFT
QECNIKHRRGRVRESEMCTGLAPVGACEGDYGGPLACFT
QECNIKHRRGRVRESEMCTGLAPVGACEGDYGGPLACFT

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

690 700 710 720
.....|.....|.....|.....|.....|.....
HNCWVLEGIIIPNRVCARSWPVAFTRVSVFVDWIHKVMR
HNCWVLEGIIIPNRVCARSWPVAFTRVSVFVDWIHKVMR
HNCWVLEGIIIPNRVCARSWPVAFTRVSVFVDWIHKVMR
HNCWVLEGIIIPNRVCARSWPVAFTRVSVFVDWIHKVMR
HNCWVLEGIIIPNRVCARSWPVAFTRVSVFVDWIHKVMR
HNCWVLEGIIIPNRVCARSWPVAFTRVSVFVDWIHKVMR
HNCWVLEGIIIPNRVCARSWPVAFTRVSVFVDWIHKVMR

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

LG (SEQ ID NO:16)
LG (SEQ ID NO:51)
LG (SEQ ID NO:52)
LG (SEQ ID NO:53)
-- (SEQ ID NO:54)
LE (SEQ ID NO:55)

Applicants: Guo
U.S.S.N.: 09/981,151

At pages 70, please replace Table 5E with the following:

Table 5E. Domain Analysis of NOV5

gnl|Pfam|pfam00051, kringle, Kringle domain. Kringle domains have been found in plasminogen, hepatocyte growth factors, prothrombin, and apolipoprotein A. Structure is disulfide-rich, nearly all-beta. (SEQ ID NO:85)
CD-Length = 79 residues, 100.0% aligned
Score = 117 bits (292), Expect = 3e-27

Query: 191 CVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPF-EPGKFLDQGLDDNYCRNPDGSERP 249
| ||| ||| |||| ||||| | ||+| | ++ +|| +||| ||| |||
Sbjct: 1 CYHGNGENYRGTA TTESGAPCQRWDSQTPHRHSKYTPERYPAKGLGENYCRNPDGDERP 60

Query: 250 WCYTTDPQIEREFCDLPRC 268 (of SEQ ID NO:16)
||| ||| ++ | +|| +|||
Sbjct: 61 WCYTTDPRVRWEYCDIPRC 79 (SEQ ID NO:85)

At pages 71, please replace Table 5F, with the following:

Table 5F. Domain Analysis of NOV5

gnl|Pfam|pfam00051, kringle, Kringle domain. Kringle domains have been found in plasminogen, hepatocyte growth factors, prothrombin, and apolipoprotein A. Structure is disulfide-rich, nearly all-beta. (SEQ ID NO:85)
CD-Length = 79 residues, 100.0% aligned
Score = 112 bits (279), Expect = 9e-26

Query: 283 CFRGKGEgyrgTANTTTAGVPCQRWDAQIPHQHRF-TPEKYACKDLRENFCRNPDGSEAP 341
|+ | || ||||| +|| +| ||||| +| ||+| ||| +| | | ||| +||| |||
Sbjct: 1 CYHGNGENYRGTA TTESGAPCQRWDSQTPHRHSKYTPERYPAKGLGENYCRNPDGDERP 60

Query: 342 WCFTLRPGMRAAFCYQIRRC 361 (of SEQ ID NO:16)
||+| | +| +| |||
Sbjct: 61 WCYTTDPRVRWEYC-DIPRC 79 (SEQ ID NO:85)

At pages 71, please replace Table 5G with the following:

Table 5G. Domain Analysis of NOV5	
gnl Pfam pfam00051, kringle, Kringle domain. Kringle domains have been found in plasminogen, hepatocyte growth factors, prothrombin, and apolipoprotein A. Structure is disulfide-rich, nearly all-beta. (SEQ ID NO:85)	
CD-Length = 79 residues, 100.0% aligned	
Score = 104 bits (259), Expect = 2e-23	

Query:	110	CIMNNGVGYRGTMTTVGGLPCQAWSHKFPNDH-KYTPT--LRNGLEENFCRNPDPGG	166
		+ + + +	
Sbjct:	1	CYHGNGENYRGTAATTESGAPCQRWDSQTPHRHSKYTPERYPAKGLGENYCRNPDGDE-R	59
Query:	167	PWCYTTPAVRFQSCGIKSC	186 (of SEQ ID NO:16)
		+ +	
Sbjct:	60	PWCYTTPRVRWEYCDIPRC	79 (SEQ ID NO:79)

At pages 71-72, please replace Table 5H with the following:

Table 5H. Domain Analysis of NOV5	
gnl Smart smart00130, KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides. (SEQ ID NO:86)	
CD-Length = 83 residues, 97.6% aligned	
Score = 111 bits (278), Expect = 1e-25	

Query:	191	CVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYCRNPDG-SERP	249
		+ + + + +	
Sbjct:	3	CYAGNGESYRGTAATTKSGKPCQRWDSQTPHLHRFTPERFPGLGLEHNYCRNPDGDSEGP	62
Query:	250	WCYTTPQIEREFCDLPRCGS	270 (of SEQ ID NO:16)
		+ + + +	
Sbjct:	63	WCYTTPNVRWEYCDIPQCES	83 (SEQ ID NO:)

At pages 72, please replace Table 5I with the following:

Table 5I. Domain Analysis of NOV5

~~gnl|Smart|smart00130~~, KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides. (SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 106 bits (265), Expect = 4e-24

Query: 108 RTCIMNNGVGYRGTMTTVGGLPCQAWSHKFPNDHKYTPTLRN--GLEENFCRNPDGDPG 165
| | || ||| +|| | || | + | + | ++|| || | +|||||
Sbjct: 1 RDCYAGNGESYRGTAATTKSGKPCQRWDSQTPHLHRFTPERFPPELGLEHNYCRNPDG DSE 60

Query: 166 GPWCYTTPAVRFQSCGIKSC 186 (of SEQ ID NO:16)
||||||| ||++ | | |
Sbjct: 61 GPWCYTTPNVRWEYCDIPQC 81 (SEQ ID NO:86)

At pages 72, please replace Table 5J with the following:

Table 5J. Domain Analysis of NOV5

~~gnl|Smart|smart00130~~, KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides. (SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 104 bits (260), Expect = 1e-23

Query: 283 CFRGKGEGYRGTAATTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDG-SEAP 341
| + | || ||||| +|| +| ||||| +| || ||||| ++ | | +||||| || |
Sbjct: 3 CYAGNGESYRGTAATTKSGKPCQRWDSQTPHLHRFTPERFPPELGLEHNYCRNPDG DSEGP 62

Query: 342 WCFTLRPGMRAAFQYQIRRCTD 363 (of SEQ ID NO:16)
||+| | +| +| | +|
Sbjct: 63 WCYTTPNVRWEYCD-IPQCES 83 (SEQ ID NO:86)

At pages 72-73, please replace Table 5K with the following:

Table 5K. Domain Analysis of NOV5

~~gnl|Smart|smart00020~~, Tryp_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues. (SEQ ID NO:87)
CD-Length = 230 residues, 79.1% aligned
Score = 110 bits (274), Expect = 3e-25

```

Query:  504  PLTGYEVWLGTLFQNPQHGEPSLQRPVAKMVCGPSGSQ-----LVLLKLERSVTLNQR  557
          +  |  ||+  +          |  |  |++  |+  +          +  |||  |||+
Sbjct:  49   APSSIRVRLGSHDLSSGEET---QTVKVSIVHPNPNSTYDNDIALLLKLSEPVTLSDT  105

Query:  558  VALICLPPEWYVVPVPGTKCEIAGWGETKGTG--NDTVLNVALLNVISNQEENIKHRGR--  613
          |  |||  |  ||  ||  |  ++|||  |  +          |  +  ++||  |  +  |
Sbjct:  106  VRPICLPSSGYNVPAGTTCTVSGWGRTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPA  165

Query:  614  -----GDYGGPLACFTHNCWVLEGIIIPNRV-CARSCWPAVFTRVS  653
          ||  |||  |  ||  ||+  |||  |  |  +|||
Sbjct:  166  ITDNMLCAGGLEGGKDACQGDGGPLVC-NDPRWVLVGIVSWGSGYGCARPKNKPGVYTRVS  224

Query:  654  VFVDWI  659  (of SEQ ID NO:16)
          ++|||
Sbjct:  225  SYLDWI  230  (SEQ ID NO:87)

```

At pages 73, please replace 5L with the following:

Table 5L. Domain Analysis of NOV5

~~gnl|Pfam|pfam00089~~, trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*). (SEQ ID NO:88)
CD-Length = 217 residues, 77.9% aligned
Score = 92.0 bits (227), Expect = 9e-20

```

Query:  508  YEVWLGTLFQNPQHGEPSLQRPVAKMV----CGPSGSQLVLLKLERSVTLNQRVALICL  563
          |  ||  |  |  +  |+  |  |++  |  +  +  |||+  |||  |  |||
Sbjct:  49   VRVVLGE--HNLGTTEGTEQKFDVKKIIVHPNPNPTNDIALLLKLKSPVTLGDTVVPICL  106

Query:  564  PPEWYVVPVPGTKCEIAGWGETKGTGNDTVLNVALLNVISNQEENIKHRG-----  612
          |  +  |  ||  |  ++|||  ||  |  |  ++  ++|  +  |  +  |
Sbjct:  107  PSASSDLPVGTTCVSVSGWGRTKNLGTSDTLQEVVVPIVSRETCSRAYSAGGTVTDTMICAGA  166

Query:  613  -----RGDYGGPLACFTHNCWVLEGIIIPNRVCARSCWPAVFTRVSVFVDWI  659
          +||  |||  |  |  ||+  ||  +  |  |  +|||  ++|||
Sbjct:  167  LGGKDACQGDGGPLVCSDG---ELVGIVSWGYGCAVGNYPGVYTRVSRYLWDWI  217

Query:  (of SEQ ID NO:16)
Sbjct:  (SEQ ID NO:88)

```

At pages 73, please replace Table 5M with the following:

Table 5M. Domain Analysis of NOV5	
gnl Smart smart00473, PAN_AP, divergent subfamily of APPLE domains; Apple-like domains present in Plasminogen, C. elegans hypothetical ORFs and the extracellular portion of plant receptor-like protein kinases. Predicted to possess protein- and/or carbohydrate-binding functions. (SEQ ID NO:89) CD-Length = 79 residues, 94.9% aligned Score = 52.0 bits (123), Expect = 1e-07	

Query:	25	DFQVLRGTELQHLLHAVVPGPWQEDVADAEECAGRC-GPLMDCRAFHYNVSSHGCQLLPW	83
		+ + +	
Sbjct:	5	CFVRLPNTKL-----PDFSPIVISVASLEECAQKCLNSNCSCRSFTYNNDTKGCLLWSE	58
Query:	84	TQHSPHTRLRRSGRCDLFQKK	104 (of SEQ ID NO:16)
		+ + ++	
Sbjct:	59	SSLGDARQLLPSSGGVDYYEKI	79 (SEQ ID NO:89)

At pages 74, please replace Table 5N with the following:

Table 5N. Domain Analysis of NOV5	
gnl Pfam pfam00024, PAN, PAN domain. The PAN domain contains a conserved core of three disulphide bridges. In some members of the family there is an additional fourth disulphide bridge the links the N and C termini of the domain. The domain is found in diverse proteins, in some they mediate protein-protein interactions, in others they mediate protein-carbohydrate interactions. (SEQ ID NO:159) CD-Length = 78 residues, 76.9% aligned Score = 50.1 bits (118), Expect = 4e-07	

Query:	45	PWQEDVADAEECAGRCGPLMD-CRAFHYNVSSHGCQLLPWTQHSPHTRLRRSGRCDLFQK	103
		+ + + + ++	
Sbjct:	17	ISVVNVPSLEECAALCLEEPRVCRSFTYNNKSKQCLLKSESSGSLPRLKRPSQKVDYYEK	
Query:	(of SEQ ID NO:16)		
Sbjct:	(SEQ ID NO:159)		

At page 78 please replace Table 6C with the following:

Table 6C. BLAST results for NOV6					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13651468 ref XP-016351.1 XP 016351	similar to GASTRIN/CHOLECYST OKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK- BR) (H. sapiens) [Homo sapiens]	135	122/135 (90%)	126/135 (92%)	1e-58
gi 4557581 ref NP-01435.1 NP 001435	fatty acid binding protein 5 (psoriasis- associated); E- FABP [Homo sapiens]	135	124/135 (91%)	126/135 (92%)	1e-58
gi 13651882 ref XP-011655.5 XP 011655	fatty acid binding protein 5 (psoriasis- associated) [Homo sapiens]	135	119/135 (88%)	124/135 (91%)	6e-57
gi 13651563 ref XP-015760.1 XP 015760	similar to GASTRIN/CHOLECYST OKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK- BR) (H. sapiens) [Homo sapiens]	135	118/135 (87%)	125/135 (92%)	5e-56
gi 6648071 sp P55052 FATE BOVIN P55052	FATTY ACID- BINDING PROTEIN, EPIDERMAL (E- FABP)	135	117/135 (86%)	124/135 (91%)	1e-55

At page 79 please replace Table 6D with the following:

Table 6D Information for the ClustalW proteins

- NOV6 (SEQ ID NO:18)
- ~~gi|13651468|ref|XP-016351.1|~~ gi|13651468| XP 016351similar to
GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens] (SEQ ID NO:56)
- ~~gi|4557581|ref|NP-001435.1|~~ gi|4557581| NP 001435fatty acid binding protein 5
(psoriasis-associated); E-FABP [Homo sapiens] (SEQ ID NO:57)
- ~~gi|13651882|ref|XP-011655.5|~~ gi|13651882| XP 011655fatty acid binding protein 5
(psoriasis-associated) [Homo sapiens] (SEQ ID NO:58)
- ~~gi|13651563|ref|XP-015760.1|~~ gi|13651563| XP 015760similar to
GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens] (SEQ ID NO:59)
- ~~gi|6648071|sp|P55052|~~ FATE BOVIN gi|13651563| P55052 FATTY ACID-BINDING PROTEIN,
EPIDERMAL (E-FABP) (SEQ ID NO:60)

		10	20	30	40
NOV6				
gi 13651468	MATVQQLGGRWRLVDSKRFDEYMKELGGVGIALRKMDAMAK				
gi 4557581	MATVQQLGGRWRLVDSKGFDEYMKELGVGIALRKMGAMAK				
gi 13651882	MATVQQLGGRWRLVDSKGFDEYMKELGVGIALRKMDTAK				
gi 13651563	MATVQQLGGRWRLVDSKGFDEYMKELGVGIALRKMGAMAK				

gi 6648071	MATVQQLVGRWRLVSKGFDEYMKVGVGMALRKVGAMAK
50.....60.....70.....80
NOV6	PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi 13651468	PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi 4557581	PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi 13651882	PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi 13651563	PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi 6648071	PDCIITSDGKNLSIKTESTLKTQFSC TLGEKFEETTADG
90.....100.....110.....120
NOV6	RKTQTVCSFADGALVQH QEWDGKENTITRKLKDGKLVVVC
gi 13651468	RKTQTVCNFTD GALVQH QEWDGKENTITRKLKDGKLVVVC
gi 4557581	RKTQTVCNFTD GALVQH QEWDGKENTITRKLKDGKLVVVC
gi 13651882	RKTQTVCNFTD GALVQH QEWDGKENTITRKLKDGKLVVVC
gi 13651563	RKTQTVCNFTD GALVQH QEWDGKENTITRKLKDGKLVVVC
gi 6648071	RKTQTVCNFTD GALVQH QEWDGKENTITRKLKDGKLVVVC
130
NOV6	VMNNVACTRIYEKVE (SEQ ID NO:18)
gi 13651468	VMNNVACTRIYEKVE (SEQ ID NO:56)
gi 4557581	VMNNVTCTRIYEKVE (SEQ ID NO:57)
gi 13651882	VMNVTCTRIYEKVE (SEQ ID NO:58)
gi 13651563	VMNNVTCTRIYEKVE (SEQ ID NO:59)
gi 6648071	VMNNVTCTRIYEKVE (SEQ ID NO:60)

Page 80, please replace Table 6E with the following:

Table 6E. Domain Analysis of NOV6	
gnl Pfam pfam00061, lipocalin, Lipocalin / cytosolic fatty-acid binding protein family. Lipocalins are transporters for small hydrophobic molecules, such as lipids, steroid hormones, bilins, and retinoids. Alignment subsumes both the lipocalin and fatty acid binding protein signatures from PROSITE. This is supported on structural and functional grounds. Structure is an eight-stranded beta barrel. (SEQ ID NO:90)	
CD-Length = 145 residues, 76.6% aligned	
Score = 53.1 bits (126), Expect = 1e-08	

Query:	9	GRWRLVDSKRFDEYMK-EGGVGTALRKMDAMAK-PDCIITCDGKNLTIKTESTLKTQFSC	66
		+ + + + + +	
Sbjct:	4	GKWYLVASANFDPELKEELGVLEATRKEITPLKEGNLEIVFDGDKNGICEETFGKLEKTK	63
Query:	67	TLGEKFEETTADGRKTQTVCSFADGALVQH QEWDGKENTITRKLKDGKLVV	117
		+ + + + + + +	
Sbjct:	64	KLGVEFDYYTGDNRFVVLDTDYDNYLLVCVQKGDGNETSRTAELYGRTPEL	114
Query: (of SEQ ID NO:18)			
Sbjct: (SEQ ID NO:90)			

Applicants: Guo
U.S.S.N.: 09/981,151

At page 84 please replace Table 7C with the following:

Table 7C. BLAST results for NOV7					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 12229761 sp Q9NTQ9 CXB4_HUMAN Q9NTQ9	GAP JUNCTION BETA-4 PROTEIN (CONNEXIN 30.3) (CX30.3)	266	266/266 (100%)	266/266 (100%)	e-155
gi 544118 sp P36380 CXB5_RAT P36380	GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3)	265	230/266 (86%)	245/266 (91%)	e-132
gi 6680015 ref NP_032153.1 NP 032153	gap junction membrane channel protein beta 4; connexin 30.3 [Mus musculus]	266	230/266 (86%)	244/266 (91%)	e-131
gi 10835079 ref NP_05259.1 NP 05259	gap junction protein, beta 5 (connexin 31.1) [Homo sapiens]	273	153/226 (67%)	177/226 (77%)	3e-88
gi 4009522 gb AAC95472.1 (AF099731) AAC95472	connexin 31.1 [Homo sapiens]	273	152/226 (67%)	176/226 (77%)	1e-87

At page 85 please replace Table 7D with the following:

Table 7D. Information for the ClustalW proteins

- NOV7 (SEQ ID NO:20)
- ~~gi|12229761|sp|Q9NTQ9|CXB4_HUMAN~~ Q9NTQ9 GAP JUNCTION BETA-4 PROTEIN (CONNEXIN 30.3) (CX30.3) (SEQ ID NO:61)
- ~~gi|544118|sp|P36380|CXB5_RAT~~ Q9NTQ9 GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3) (SEQ ID NO:62)
- ~~gi|6680015|ref|NP_032153.1|~~ NP 032153 gap junction membrane channel protein beta 4; connexin 30.3 [Mus musculus] (SEQ ID NO:63)
- ~~gi|10835079|ref|NP_05259.1|~~ NP 05259 gap junction protein, beta 5 (connexin 31.1) [Homo sapiens] (SEQ ID NO:64)
- ~~gi|4009522|gb|AAC95472.1|~~ AAC95472 (AF099731) connexin 31.1 [Homo sapiens] (SEQ ID NO:65)

	10	20	30	40
NOV7
gi 12229761	MNWAFLQGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVAA			
gi 544118	MNWAFLQGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVAA			
gi 6680015	MNWAFLQGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVAA			
gi 10835079	MNWSIFGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVTA			
gi 4009522	MNWSIFGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVTA			
	50	60	70	80
NOV7
gi 12229761	EEVWDDEQKDFVCNTKQPGCPNVCYDEFFPVSHVRLWALQ			

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi|544118|EEVWDDDEQKDFECNTKQPGCPNVCYDEFFPVSHVRLWALQ
gi|6680015|EEVWDDDEQKDFECNTKQPGCPNVCYDEFFPVSHVRLWALQ
gi|10835079|ERVWSDDEHKDFECNTRQPGCSNVCEDEFFPVSHVRLWALQ
gi|4009522|XRVWSDDEHKDFECNTRQPGCSNVCEDEFFPVSHVRLWALQ
```

```
          90      100      110      120
.....|.....|.....|.....|.....|.....|
NOV7    LILVTCPSLLVMHVAYREERERKHLKHGPNAPSLYDNL
gi|12229761|LILVTCPSLLVMHVAYREERERKHLKHGPNAPSLYDNL
gi|544118|LILVTCPSLLVMHVAYREERERKHLKHGPNAPSLYDNL
gi|6680015|LILVTCPSLLVMHVAYREERERKHLKHGPNAPSLYDNL
gi|10835079|LILVTCPSLLVMHVAYREVOEKRHREAHGENSGRLYLNP
gi|4009522|LILVTCPSLLVMHVAYREVOEKRHREAHGENSGRLYLNP
```

```
          130      140      150      160
.....|.....|.....|.....|.....|.....|
NOV7    SKKRGGGLWWTYLLSLIFKAAVDAGFLYIEHRLYKDYDMPR
gi|12229761|SKKRGGGLWWTYLLSLIFKAAVDAGFLYIEHRLYKDYDMPR
gi|544118|SKKRGGGLWWTYLLSLIFKAAVDAGFLYIEHRLYKDYDMPR
gi|6680015|SKKRGGGLWWTYLLSLIFKAAVDAGFLYIEHRLYKDYDMPR
gi|10835079|GKKRGGGLWWTYVCSLVEKASVDIAFLYVEHSFYPKVITPP
gi|4009522|GKKRGGGLWWTYVCSLVEKASVDIAFLYVEHSFYPKVITPP
```

```
          170      180      190      200
.....|.....|.....|.....|.....|.....|
NOV7    VVACSVPCPHTVDCYISRPTTEKKVFTYFMVITAAICILL
gi|12229761|VVACSVPCPHTVDCYISRPTTEKKVFTYFMVITAAICILL
gi|544118|VVACSVPCPHTVDCYISRPTTEKKVFTYFMVITAAICILL
gi|6680015|VVACSVPCPHTVDCYISRPTTEKKVFTYFMVITAAICILL
gi|10835079|VVKCHADPCPNIVDCIISKPSSEKNLFTLEFVATAAICILL
gi|4009522|VVKCHADPCPNIVDCIISKPSSEKNLFTLEFVATAAICILL
```

```
          210      220      230      240
.....|.....|.....|.....|.....|.....|
NOV7    NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
gi|12229761|NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
gi|544118|NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
gi|6680015|NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
gi|10835079|NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
gi|4009522|NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
```

```
          250      260      270
.....|.....|.....|.....|.....|.....|
NOV7    YVLSQGG---HPEDGNSVLMKAGSAPVDAGGYP (SEQ ID NO:20)
gi|12229761|YVLSQGG---HPEDGNSVLMKAGSAPVDAGGYP (SEQ ID NO:61)
gi|544118|YVLSQGG---HPEDGNSVLMKAGSAPVDAGGYP (SEQ ID NO:62)
gi|6680015|YVLSQGG---HPEDGNSVLMKAGSAPVDAGGYP (SEQ ID NO:63)
gi|10835079|DDLISGOLIFLGSDSHPPPLPDRPRDHVKKTL- (SEQ ID NO:64)
gi|4009522|DDLISGOLIFLGSDSHPPPLPDRPRDHVKKTL- (SEQ ID NO:65)
```

At page 86 please replace Table 7E with the following:

Applicants: Guo
U.S.S.N.: 09/981,151

Table 7E. Domain Analysis of NOV7

~~gnl|Pfam|pfam00029~~, connexin, Connexin. (SEQ ID NO:91)
CD-Length = 218 residues, 100.0% aligned
Score = 318 bits (814), Expect = 3e-88

```

Query:  1  MNWAFLLQGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVAEEVWDDEQKDFVCNTKQPGC  60
        |||+||| || |||+|| + +|||+|||+||| ||| || ||| |||+|||
Sbjct:  1  MDWSFLGRLLLEGVNHSTAIGKIWLSVLFIFRILVLGVAAESVWGDEQSDVCNTQQPGC  60

Query: 61  PNVCYDEFFPVSHVRLWALQLILVTCPSLLVVMHVAYREERERKHHLKHGPNAPSLYDNL 120
        |||+|||+||| ||| ||| + ||| + ||| ||| |  ++ ||
Sbjct: 61  ENVCYDQFFPISHVRLWVLQLIFVSTPSLLYLGHVAYRVRREEKLREKEEEHSGLYSEE 120

Query: 121 SKK-----RGGLWWTYLLSLIFKAAVDAGFLYIFHRLYKDYDMPRVVACSVEPC 169
        +|| ||| |||+ |||+ + ||| + || + | + || ||
Sbjct: 121 AKKRCGSEDGKVRIRGGLWWTYVFSIIFKSIFEVGFLYGQYLLY-GFTMSPLVVCSRAPC 179

Query: 170 PHTVDCYISRPTTEKKVFTYFMVTTAAICILLNLSEVFYL 208 (of SEQ ID NO:20)
        |||+|||+||| +| ||+ +||+|||+|||
Sbjct: 180 PHTVDCFVSRPTEKTIFIVFMLVVSACILLNLAEFLYL 218 (SEQ ID NO:91)

```

At page 87, please replace Table 7F with the following:

Table 7F. Domain Analysis of NOV7

~~gnl|Smart|smart00037~~, CNX, Connexin homologues; Connexin channels participate in the regulation of signaling between developing and differentiated cell types. (SEQ ID NO:160)
CD-Length = 34 residues, 100.0% aligned
Score = 79.0 bits (193), Expect = 3e-16

```

Query:  42  EVWDDEQKDFVCNTKQPGCPNVCYDEFFPVSHVR  75  (of SEQ ID NO:20)
        || ||| || |||+||| |||+|||+|||
Sbjct:  1  SVWGDEQSDFTCNTQQPGCENVCYDQFFPISHVR  34  (SEQ ID NO:160)

```

At page 100, please replace Table 9C with the following:

Table 9C. BLAST results for NOV9

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13591536 emb CAC36351.1 CAC36351 (AL109613)	dJ1033H22.1 (KIAA0554 protein) [Homo sapiens]	434	373/430 (86%)	375/430 (86%)	0.0

Applicants: Guo
U.S.S.N.: 09/981,151

gi 8923249 ref NP_060207.1 NP 060207	hypothetical protein FLJ20275 [Homo sapiens]	330	328/330 (99%)	329/330 (99%)	e-175
gi 10435680 dbj BAB14638.1 BAB14638 (AK023681)	unnamed protein product [Homo sapiens]	592	319/595 (53%)	432/595 (71%)	e-160
gi 13936547 gb AAK49824.1 AF265550.1 AAK49824 (AF265550)	formin-binding protein 17 [Homo sapiens]	679	307/624 (49%)	422/624 (67%)	e-148
gi 3043632 dbj BAA25480.1 BAA25480 (AB011126)	KIAA0554 protein [Homo sapiens]	674	307/624 (49%)	422/624 (67%)	e-148

At page 100 please replace Table 9D with the following:

Table 9D. ClustalW Analysis of NOV9

- 1) Novel NOV9 (SEQ ID NO:24)
- 3) ~~gi|13591536|emb|CAC36351.1|~~ CAC36351 ~~gi|13591536|~~ (AL109613) dJ1033H22.1 (KIAA0554 protein) [Homo sapiens] (SEQ ID NO:66)
- 4) ~~gi|8923249|ref|NP_060207.1|~~ NP 060207 ~~gi|8923249|~~ hypothetical protein FLJ20275 [Homo sapiens] (SEQ ID NO:67)
- 5) ~~gi|10435680|dbj|BAB14638.1|~~ BAB14638 ~~gi|10435680|~~ (AK023681) unnamed protein product [Homo sapiens] (SEQ ID NO:68)
- 6) ~~gi|13936547|gb|AAK49824.1|AF265550.1|~~ AAK49824 ~~gi|13936547|~~ (AF265550) formin-binding protein 17 [Homo sapiens] (SEQ ID NO:69)
- 7) ~~gi|3043632|dbj|BAA25480.1|~~ BAA25480 ~~gi|3043632|~~ (AB011126) KIAA0554 protein [Homo sapiens] (SEQ ID NO:70)

	10	20	30	40
NOV9
gi 13591536	-----	-----	-----	-----
gi 8923249	-----	-----	-----	-----
gi 10435680	-----	-----	-----	-----
gi 13936547	LWNGGEEEEPPRRPRARSCEPEEAARTPGFPPSRGSRGAKG			
gi 3043632	-----EEEPRRPRARSCEPEEAARTPGFPPSRGSRGAKG			
	50	60	70	80
NOV9
gi 13591536	-----	-----	-----	-----
gi 8923249	-----	-----	-----	-----
gi 10435680	-----	-----	-----	-----
gi 13936547	SPGRGTREPRPPRGAPLRVPCTMSWGTELWDQFDNLEKHT			
gi 3043632	SPGRGTREPRPPRGAPLRVPCTMSWGTELWDQFDNLEKHT			
	90	100	110	120
NOV9	QWGIDFLERYAKFVKERIEIEQNYAKQLRNLSKKYCPKRS			
gi 13591536	-----	-----	-----	-----
gi 8923249	-----	-----	-----	-----
gi 10435680	QWGIDILEKYIKFVKERIEIELSYAKQLRNLSKKYQPKEN			
gi 13936547	QWGIDILEKYIKFVKERIEIELSYAKQLRNLSKKYQPKEN			
gi 3043632	QWGIDILEKYIKFVKERIEIELSYAKQLRNLSKKYQPKEN			

Applicants: Guo
U.S.S.N.: 09/981,151

```

      130      140      150      160
      |-----|-----|-----|-----|
NOV9  SKDEE-PRETSCVAFFNINLNEINDYAGOREVVAEEMAHRV
gi | 13591536 |
gi | 8923249 |
gi | 10435680 | SKEEEEYKYTSCKAFISNLNEINDYAGOREVTSENMASOI
gi | 13936547 | SKEEEEYKYTSCKAFISNLNEINDYAGOREVTSENMASOI
gi | 3043632 | SKEEEEYKYTSCKAFISNLNEINDYAGOREVTSENMASOI

```

```

      170      180      190      200
      |-----|-----|-----|-----|
NOV9  YGELMRYAEDLKTERKMLQEGRKAQQHDMCWKONGNSK
gi | 13591536 |
gi | 8923249 |
gi | 10435680 | IVDLARYVQELKQERKSNFHDGRKAQQHETCWKQLESSEK
gi | 13936547 | IVDLARYVQELKQERKSNFHDGRKAQQHETCWKQLESSEK
gi | 3043632 | IVDLARYVQELKQERKSNFHDGRKAQQHETCWKQLESSEK

```

```

      210      220      230      240
      |-----|-----|-----|-----|
NOV9  GKFERECREAEKAQOSYERLDNDTNATKADVENAKQOOLNI
gi | 13591536 |
gi | 8923249 |
gi | 10435680 | RRFERECREADRAQQYFEKMDADINVTKADVEKARQQAQI
gi | 13936547 | RRFERECREADRAQQYFEKMDADINVTKADVEKARQQAQI
gi | 3043632 | RRFERECREADRAQQYFEKMDADINVTKADVEKARQQAQI

```

```

      250      260      270      280
      |-----|-----|-----|-----|
NOV9  RTHMADENKNAYAAQLQNFNGEQHGHFYVVIPIYKQIQE
gi | 13591536 |
gi | 8923249 |
gi | 10435680 | RHOMAEADSKADYSSILOKFNHEQHGHFYVTHIPNIFOKIQE
gi | 13936547 | RHOMAEADSKADYSSILOKFNHEQHGHFYVTHIPNIFOKIQE
gi | 3043632 | RHOMAEADSKADYSSILOKFNHEQHGHFYVTHIPNIFOKIQE

```

```

      290      300      310      320
      |-----|-----|-----|-----|
NOV9  MDERRTQQLSECYRGFADSERKVIPIISKCLEGMMLAAKS
gi | 13591536 |
gi | 8923249 |
gi | 10435680 | MEERRIVRMGESMKTVAEVDROVPIIIGKCLDGIYKAAES
gi | 13936547 | MEERRIVRMGESMKTVAEVDROVPIIIGKCLDGIYKAAES
gi | 3043632 | MEERRIVRMGESMKTVAEVDROVPIIIGKCLDGIYKAAES

```

```

      330      340      350      360
      |-----|-----|-----|-----|
NOV9  VDERRDSQMVVDSEKSGFEPPGDFPFEDYSQHHTYRTISDG
gi | 13591536 |
gi | 8923249 |
gi | 10435680 | IDOKNDSQVIEEAYKSGFEPPGDIEFEDYTQPMKRTVSDN
gi | 13936547 | IDOKNDSQVIEEAYKSGFEPPGDIEFEDYTQPMKRTVSDN
gi | 3043632 | IDOKNDSQVIEEAYKSGFEPPGDIEFEDYTQPMKRTVSDN

```

```

      370      380      390      400
      |-----|-----|-----|-----|
NOV9  MISASKOESGKMDAKTPVGKAKGKLWLFCKKPK
gi | 13591536 |
gi | 8923249 |
gi | 10435680 | SPNSNRGE-GKPDLEKFG-GKSKGKLWPFIKKN
gi | 13936547 | SPNSNRGE-GKPDLEKFG-GKSKGKLWPFIKKNKLMSLLTS
gi | 3043632 | SPNSNRGE-GKPDLEKFG-GKSKGKLWPFIKKNKLMSLLTS

```

```

      410      420      430      440

```

Applicants: Guo
U.S.S.N.: 09/981,151

NOV9

```
.....|.....|.....|.....|.....|.....|.....|.....|
--QSPPLTPTSLFTSSTPNGSOFLTFSIEPVHYCMNEIKT
gi | 13591536 |
gi | 8923249 |
gi | 10435680 |
gi | 13936547 |
gi | 3043632 |
```

NOV9

```
450      460      470      480
.....|.....|.....|.....|.....|.....|.....|.....|
-----G-----PALEDFSHLPPEQRRKKLQQ
gi | 13591536 |
gi | 8923249 |
gi | 10435680 |
gi | 13936547 |
gi | 3043632 |
```

NOV9

```
490      500      510      520
.....|.....|.....|.....|.....|.....|.....|.....|
RIDEINREIQEKESDQKDAENKMKDVYEKDPOMGDPGSLQP
gi | 13591536 |
gi | 8923249 |
gi | 10435680 |
gi | 13936547 |
gi | 3043632 |
```

NOV9

```
530      540      550      560
.....|.....|.....|.....|.....|.....|.....|.....|
KLAETMNNIDRLRMEIHKNEAWLSEVEGKTGGRGD--RRH
gi | 13591536 |
gi | 8923249 |
gi | 10435680 |
gi | 13936547 |
gi | 3043632 |
```

NOV9

```
570      580      590      600
.....|.....|.....|.....|.....|.....|.....|.....|
SSDIN-----HLVTQGRESPEGSYTDDANQEVGRPPOQ
gi | 13591536 |
gi | 8923249 |
gi | 10435680 |
gi | 13936547 |
gi | 3043632 |
```

NOV9

```
610      620      630      640
.....|.....|.....|.....|.....|.....|.....|.....|
HGHHNEFDDEFEDDDPLPAIGHCKATYPFDGHNEGTLAMK
gi | 13591536 |
gi | 8923249 |
gi | 10435680 |
gi | 13936547 |
gi | 3043632 |
```

NOV9

```
650      660      670      680
.....|.....|.....|.....|.....|.....|.....|.....|
EGEVLYHIEEDKGDGWTRARRONGEEGYVPTSYPEDVILEK
gi | 13591536 |
gi | 8923249 |
gi | 10435680 |
gi | 13936547 |
gi | 3043632 |
```

.....|.....

Applicants: Guo
U.S.S.N.: 09/981,151

NOV9	NSKGS----	(SEQ ID NO:24)
gi 13591536	NSKGAVTYI	(SEQ ID NO:66)
gi 8923249	NSKGS----	(SEQ ID NO:67)
gi 10435680	NAKGAKTYI	(SEQ ID NO:68)
gi 13936547	NAKDS----	(SEQ ID NO:69)
gi 3043632	NAKDS----	(SEQ ID NO:70)

At page 103, please replace Table 9E with the following:

Table 9E. Domain Analysis of NOV9	
gnl Smart smart00326,	SH3, Src homology 3 domains; Src homology 3 (SH3) domains bind to target proteins through sequences containing proline and hydrophobic amino acids. Pro-containing polypeptides may bind to SH3 domains in 2 different binding orientations. (SEQ ID NO:92)
CD-Length = 59 residues, 88.1% aligned	
Score = 64.7 bits (156), Expect = 1e-11	

Query:	484	HCKAIYPFDGHNEGTLAMKEGEVLYIIIEEDKGDGWTRARRQNGEEGYVPTSYI	536
		+ + + + + + +++ ++ + + + ++ +	
Sbjct:	4	QVRALYDYTAQDPDELSFKKGDIIITVLEKS-DDGWWKGR LGTGKEGLFPSNYV	55

Query: (of SEQ ID NO:24)

Sbjct: (SEQ ID NO:92)

At page 104, please replace Table 9F with the following:

Table 9F. Domain Analysis of NOV9	
gnl Pfam pfam00018,	SH3, SH3 domain. SH3 (Src homology 3) domains are often indicative of a protein involved in signal transduction related to cytoskeletal organization. First described in the Src cytoplasmic tyrosine kinase. The structure is a partly opened beta barrel. (SEQ ID NO:93)
CD-Length = 57 residues, 91.2% aligned	
Score = 63.5 bits (153), Expect = 3e-11	

Query:	486	KAIYPFDGHNEGTLAMKEGEVLYIIIEEDKGDGWTRARRQNGEEGYVPTSYID	537
		A+Y + L+ K+G+++ ++E+ GW + R + +EG +P++Y++	
Sbjct:	4	VALYDYQARESDELSFKKGDIIIVLEKSDDGGWWKGR LKGTKEGLIPSNYVE	55

Query: of SEQ ID NO:24)

Sbjct: (SEQ ID NO:93)

At page 104, please replace Table 9 with the following:

Table 9G. Domain Analysis of NOV9	
gnl Smart smart000557, FCH, Fes/CIP4 homology domain; Alignment extended from original report. Highly alpha-helical. Also known as the RAEYL motif or the S. pombe Cdc15 N-terminal domain. (SEQ ID NO:94) CD-Length = 91 residues, 97.8% aligned Score = 58.2 bits (139), Expect = 1e-09	

Query:	1	MSWGTELWDQFDSLKDHTQWGIDFLERYAKFVKERIEIEQNYAKQLRNLVKKYCPKRSSK	60
		+ + ++ + ++ + + + +	
Sbjct:	1	MGFWSELDDGFEALLSRLKNGRLLEDLKKFMRERAKIEEEYAKKLQKLSKK--LRAVRD	58
Query:	61	DEEPRFTSCVAFFNILNELNDYAGQREVVAE	91 (of SEQ ID NO:24)
		+ + + + ++	
Sbjct:	59	TESELGSLRKAWEVLLSETDALAKQHLQLSE	89 (SEQ ID NO:94)

At page 104, please replace Table 9H with the following:

Table 9H. Domain Analysis of NOV9	
gnl Pfam pfam006117, FCH, Fes/CIP4 homology domain. Alignment extended from. Highly alpha-helical. (SEQ ID NO:95) CD-Length = 94 residues, 97.9% aligned Score = 40.0 bits (92), Expect = 3e-04	

Query:	1	MSWGTELWDQ-FDSLKDHTQWGIDFLERYAKFVKERIEIEQNYAKQLRNLVKKYCPKRSS	59
		+ + + + + + + + + + +	
Sbjct:	1	MGFGSELCPGCHKALLSRQDNELRLLEEMKKFMAERAKIEKEYAGKLQHLQAQVGKGPAT	60
Query:	60	KDEEPRFTSCVAFFNILNELNDYAGQREVVAE	91 (of SEQ ID NO:24)
		+ + ++ + + ++	
Sbjct:	61	AEGEDELSSLKSWAVILSETEQQSKIHLQISE	92 (SEQ ID NO:95)

At page 113 please replace Table 10F with the following:

Table 10F. BLAST results for NOV10a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13540535 ref NP-110397.1 NP 110397	transmembrane protease, serine 5; spinesin [Homo sapiens]	457	452/463 (97%)	453/463 (97%)	0.0
gi 13878822 sp Q9ER04 TMS5-MOUSE Q9ER04	TRANSMEMBRANE PROTEASE, SERINE 5 (SPINESIN)	455	360/461 (78%)	394/461 (85%)	0.0
gi 13507652 ref NP-109634.1 NP 109634	transmembrane protease, serine 5 (spinesin) [Mus musculus]	445	354/451 (78%)	388/451 (85%),	0.0
gi 14770563 ref XP-041427.1 XP 041427	transmembrane protease, serine 5 [Homo sapiens]	398	354/362 (97%)	355/362 (97%)	0.0
gi 12248777 dbj BAB20276.1 BAB20276 (AB016229)	type 2 spinesin [Mus musculus]	311	260/317 (82%)	281/317 (88%)	e-146

At page 114 please replace Table 10G with the following:

Table 10G. ClustalW Analysis of NOV10

- 1) Novel NOV10a (SEQ ID NO:27)
- 2) Novel NOV10b (SEQ ID NO:29)
- 4) ~~gi|13540535|ref|NP-110397.1|~~ NP 110397 ~~gi|13540535|~~ transmembrane protease, serine 5; spinesin [Homo sapiens] (SEQ ID NO:71)
- 5) ~~gi|13878822|sp|Q9ER04|TMS5-MOUSE~~ Q9ER04 ~~gi|13878822|~~ TRANSMEMBRANE PROTEASE, SERINE 5 (SPINESIN) (SEQ ID NO:72)
- 6) ~~gi|13507652|ref|NP-109634.1|~~ NP 109634 ~~gi|13507652|~~ transmembrane protease, serine 5 (spinesin) [Mus musculus] (SEQ ID NO:73)
- 7) ~~gi|14770563|ref|XP-041427.1|~~ XP 041427 ~~gi|14770563|~~ transmembrane protease, serine 5 [Homo sapiens] (SEQ ID NO:74)
- 8) ~~gi|12248777|dbj|BAB20276.1|~~ BAB20276 ~~gi|12248777|~~ (AB016229) type 2 spinesin [Mus musculus] (SEQ ID NO:75)

	10	20	30	40
NOV10a	MSLMLDDQPPMEAGYAEEGPGPGIFRAEPGDQHPISQAV			
NOV10b	MSLMLDDQPPMEAGYAEEGPGPGIFRAEPGDQHPISQAV			
gi 13540535	MSLMLDDQPPMEAGYAEEGPGPGIFRAEPGDQHPISQAV			
gi 13878822	MSPTLDDQSPMEIRCTEEGAGPGIFRMELGDORQSISQSQ			
gi 13507652	-----MEIRCTEEGAGPGIFRMELGDORQSISQSQ			
gi 14770563	MSLMLDDQPPMEAGYAEEGPGPGIFRAEPGDQHPISQAV			
gi 12248777	-----			
	50	60	70	80
NOV10a	CWRSMRRGCAVLGALGLLAGAGVGSWLLVLVYLCPAASQPI			
NOV10b	CWRSMRRGCAVLGALGLLAGAGVGSWLLVLVYLCPAASQPI			
gi 13540535	CWRSMRRGCAVLGALGLLAGAGVGSWLLVLVYLCPAASQPI			
gi 13878822	RWCCLERGCVILGVLGLLAGAGIASWLLVLVYLWPAASPSI			
gi 13507652	RWCCLERGCVILGVLGLLAGAGIASWLLVLVYLWPAASPSI			
gi 14770563	CWRSMRRGCAVLGALGLLAGAGVGSWLLVLVYLCPAASQPI			
gi 12248777	-----			

Applicants: Guo
U.S.S.N.: 09/981,151

	90	100	110	120
NOV10a	SGTLQDEEETLSCSEASAEFALLPLPKTVSFRINSEDFL			
NOV10b	SGTLQDEEETLSCSEASAEFALLPLPKTVSFRINSEDFL			
gi 13540535	SGTLQDEEETLSCSEASAEFALLPLPKTVSFRINSEDFL			
gi 13878822	SGTLQDEEETLSCSEASAEFALLPLPKTVSFRINSEDFL			
gi 13507652	SGTLQDEEETLSCSEASAEFALLPLPKTVSFRINSEDFL			
gi 14770563	SGTLQDEEETLSCSEASAEFALLPLPKTVSFRINSEDFL			
gi 12248777	SGTLQDEEETLSCSEASAEFALLPLPKTVSFRINSEDFL			

	130	140	150	160
NOV10a	LEAQVRDQPRWLLVCHEGWSPALGLOICWSLGHERLTHHK			
NOV10b	LEAQVRDQPRWLLVCHEGWSPALGLOICWSLGHERLTHHK			
gi 13540535	LEAQVRDQPRWLLVCHEGWSPALGLOICWSLGHERLTHHK			
gi 13878822	LEAQVRDQPRWLLVCHEGWSPALGLOICWSLGHERLTHHK			
gi 13507652	LEAQVRDQPRWLLVCHEGWSPALGLOICWSLGHERLTHHK			
gi 14770563	LEAQVRDQPRWLLVCHEGWSPALGLOICWSLGHERLTHHK			
gi 12248777	LEAQVRDQPRWLLVCHEGWSPALGLOICWSLGHERLTHHK			

	170	180	190	200
NOV10a	GVNLDIKLNSQEFALSPRLGGFEEAWOPSRTEAVR			
NOV10b	GVNLDIKLNSQEFALSPRLGGFEEAWOP-----R			
gi 13540535	GVNLDIKLNSQEFALSPRLGGFEEAWOP-----R			
gi 13878822	GVNLDIKLNSQEFALSPRLGGFEEAWOP-----R			
gi 13507652	GVNLDIKLNSQEFALSPRLGGFEEAWOP-----R			
gi 14770563	GVNLDIKLNSQEFALSPRLGGFEEAWOP-----R			
gi 12248777	GVNLDIKLNSQEFALSPRLGGFEEAWOP-----R			

	210	220	230	240
NOV10a	NNCTSGOVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA			
NOV10b	NNCTSGOVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA			
gi 13540535	NNCTSGOVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA			
gi 13878822	NNCTSGOVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA			
gi 13507652	NNCTSGOVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA			
gi 14770563	NNCTSGOVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA			
gi 12248777	NNCTSGOVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA			

	250	260	270	280
NOV10a	SVALGFRHTCGCSVLAPRWVVTAAHCMISFRLRLSSWRV			
NOV10b	SVALGFRHTCGCSVLAPRWVVTAAHCMISFRLRLSSWRV			
gi 13540535	SVALGFRHTCGCSVLAPRWVVTAAHCMISFRLRLSSWRV			
gi 13878822	SVALGFRHTCGCSVLAPRWVVTAAHCMISFRLRLSSWRV			
gi 13507652	SVALGFRHTCGCSVLAPRWVVTAAHCMISFRLRLSSWRV			
gi 14770563	SVALGFRHTCGCSVLAPRWVVTAAHCMISFRLRLSSWRV			
gi 12248777	SVALGFRHTCGCSVLAPRWVVTAAHCMISFRLRLSSWRV			

	290	300	310	320
NOV10a	HAGLVSHSAVRPHQGAVERIIPHPLYSAQNHDYDVALLR			
NOV10b	HAGLVSHSAVRPHQGAVERIIPHPLYSAQNHDYDVALLR			
gi 13540535	HAGLVSHSAVRPHQGAVERIIPHPLYSAQNHDYDVALLR			
gi 13878822	HAGLVSHSAVRPHQGAVERIIPHPLYSAQNHDYDVALLR			
gi 13507652	HAGLVSHSAVRPHQGAVERIIPHPLYSAQNHDYDVALLR			
gi 14770563	HAGLVSHSAVRPHQGAVERIIPHPLYSAQNHDYDVALLR			
gi 12248777	HAGLVSHSAVRPHQGAVERIIPHPLYSAQNHDYDVALLR			

	330	340	350	360
NOV10a	LQTAENFSDTVGAVCLPAKEQFFPKGSRWCWVSGWGHTPS			

Applicants: Guo
U.S.S.N.: 09/981,151

NOV10b

gi	13540535	LOTALNFSDTVGAVCLPAKEQEFPGKSR	CWVSGWGHTDPS
gi	13878822	LRTPINFSDTVDAVCLPAKEQEFPGSG	CWVSGWGHTDPS
gi	13507652	LRTPINFSDTVGAVCLPAKEQEFPGSG	CWVSGWGHTDPS
gi	14770563	LOTALNFSDTVGAVCLPAKEQEFPGKSR	CWVSGWGHTDPS
gi	12248777	LRTPINFSDTVDAVCLPAKEQEFPGSG	CWVSGWGHTDPS

370 380 390 400
 NOV10a HTYSSDMLQDTVPPLLSTOLCNSSCVYSGALTPRMLCAGY
 NOV10b HTYSSDMLQDTVPPLLSTOLCNSSCVYSGALTPRMLCAGY
 gi | 13540535 | HTYSSDMLQDTVPPLFSTOLCNSSCVYSGALTPRMLCAGY
 gi | 13878822 | HTSSDILQDTVPPLLSTELCNSSCVYSGALTPRMLCAGY
 gi | 13507652 | HTSSDILQDTVPPLLSTELCNSSCVYSGALTPRMLCAGY
 gi | 14770563 | H-----S-----LQLG
 gi | 12248777 | HTSSDILQDTVPPLLSTELCNSSCVYSGALTPRMLCAGY

		410	420	430	440
NOV10a		LDGRADACQGD	SGGPLVCPD	GDTWRLVG	VSWGRGCAEPN
NOV10b		LDGRADACQGD	SGGPLVCPD	GDTWRLVG	VSWGRGCAEPN
gi 13540535		LDGRADACQGD	SGGPLVCPD	GDTWRLVG	VSWGRACAEPN
gi 13878822		LDGRADACQGD	SGGPLVCP	SGDTWELVG	VSWGRGCAEPN
gi 13507652		LDGRADACQGD	SGGPLVCP	SGDTWELVG	VSWGRGCAEPN
gi 14770563		APG-----	EGGALVQHS	-----	ALQQLRVOR---SP
gi 12248777		LDGRADACQGD	SGGPLVCP	SGDTWELVG	VSWGRGCAEPN

		450	460	470	
				
NOV10a		H P G V Y A K V A E F L D W I H D T A Q V S V G A G V G Q G D F	(SEQ ID NO: 27)		
NOV10b		H P G V Y A K V A E F L D W I H D T A Q D S L L - - - - -	(SEQ ID NO: 29)		
gi 13540535		H P G V Y A K V A E F L D W I H D T A Q D S L L - - - - -	(SEQ ID NO: 71)		
gi 13878822		R P G V Y A K V A E F L D W I H D T V Q V R - - - - -	(SEQ ID NO: 72)		
gi 13507652		R P G V Y A K V A E F L D W I H D T V Q V R - - - - -	(SEQ ID NO: 73)		
gi 14770563		P P - - - - - H A L R W L P G R K G - - - - -	(SEQ ID NO: 74)		
gi 12248777		R P G V Y A K V A E F L D W I H D T V Q V R - - - - -	(SEQ ID NO: 75)		

At page 116, please replace Table 10H with the following:

Table 10H Domain Analysis of NOV10

gnl|Smart|smart00020, Tryp_SPC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues. (SEQ ID NO:96)
CD-Length = 230 residues, 100.0% aligned
Score = 266 bits (681), Expect = 2e-72

Query:	224	RIVGGQSVAPGRWPWQASVAL-GFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHA	282
		+ + + + + + + +	
Sbjct:	1	RIVGGSEANIGSFPWQVSLQYRGGRHFCGGSLSIPRWVLTAAHCVYGSAP---SSIRVRL	57
Query:	283	GLVSHSAVRPHQGALVERIIPHPLYSAQNHDYDVALRLQTALNFSDTVGA VCLPAKEQH	342
		+ + + + + + + + + +	
Sbjct:	58	GSHDLSSGEETQTVKVKVIVHPNYPSTYDNDIALLLKLEPVTLSDTV RPICLPSSGYN	117
Query:	343	FPKGSRCWVSGWGHTHPSHTYSSDMLQDTVPVPLLSTQLCNSSCVYSGALT P RMLCAGYLD	402

Applicants: Guo
U.S.S.N.: 09/981,151

Sbjct: 118 | | + | | | | | | | | | | | | + | | + | | + | | + | | | | | +
VPAGTTCTVSGWGRTSESSGSLPDTLQEVNVPISNATCRRAYSGGPAITDNMLCAGGLE 177

Query: 403 GRADACQGDSGGPLVCPDGDWRLVGVVSWGR-GCAEPNHPGVYAKVAEFLDWI 455

Sbjct: 178 | | | | | | | | | | | | + | | | + | | | | | | | | | | + | + | | | |
GGKDACQGDSGGPLVC-NDPRWVLVGIVSWGSGYGCARPKNKPGVYTRVSSYLDWI 230

Query: (of SEQ ID NO:27)

Sbjct: (SEQ ID NO:96)

At page 116, please replace Table 10I with the following:

Table 10I. Domain Analysis of NOV10

gnl|Pfam|pfam00089, trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*). (SEQ ID NO:97)
CD-Length = 217 residues, 100.0% aligned
core = 211 bits (538), Expect = 6e-56

Query: 225 IVGGQSVAPGRWPWQASVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHAGL 284

Sbjct: 1 | | | | + | + | | | + + | | | | + + | + | | | | + | | | | |
IVGGREAAQAGSFPWQVSLQVSSGHFCGSLISENWVLTAAHCVSG-----ASSVRVVLGE 55

Query: 285 VSHSAVRPH-QGALVERIIPHPLYSAQNHDYDVALLRQLTALNFSDTVGA VCLPAKEQHF 343

Sbjct: 56 + | | | + + | | | + | + | | + | + + | | | + | | | +
HNLGTTEGTEQKFDVKKIIVHPNYPDT--NDIALCLKSPVTLGDTV RPICLPSASSDL 113

Query: 344 PKGSRWVSGWGH THPSHTYSSDMLQDTVVP LLSTQLCNSSCVYSGALT PRMLCAGYLDG 403

Sbjct: 114 | | + | | | | | | + + | | | + | | | + + | + | | + | | + | | | | |
PVGTTCSVSGWGRTK--NLGTS DTLQEVVVPISRETCSA--YGGTVTDTMICAGALGG 169

Query: 404 RADACQGDSGGPLVCPDGDWRLVGVVSWGRGCAEPNHPGVYAKVAEFLDWI 455

Sbjct: 170 + | | | | | | | | | | | | | | | + | | | | | | | | + | + | + | | | |
K-DACQGDSGGPLVCSDG---ELVGIVSWG YGCAVGNYPGVYTRVSR YLDWI 217

Query: (of SEQ ID NO:27)

Sbjct: (SEQ ID NO:97)